COMPOSITIONS AND METHODS FOR THE MODULATION OF SPHINGOLIPID METABOLISM AND/OR SIGNALING

CROSS REFERENCE TO RELATED APPLICATIONS

This application is a continuation-in-part of U.S. Application number 10/348,052, which claims the benefit of provisional application number 60/349,582, filed January 17, 2002 and U.S. Application number 10/053,510, filed January 17, 2002, all applications incorporated herein by reference in their entirety.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

This invention was made with government support under Grant No. 1R01CA77528 awarded by the National Institutes of Health. The government has certain rights in this invention.

BACKGROUND OF THE INVENTION

Field of the Invention

The present invention relates generally to cancer detection and therapy. The invention is more particularly related to polynucleotides encoding polypeptides involved in the metabolism of sphingolipids, polypeptides, and to agents that modulate the expression and/or activity of such polypeptides. Such agents may be used, for example, to diagnose and/or treat cancers such as breast, colon, uterus, stomach, ovary, lung, kidney and rectum cancer, the diagnosis and treatment of muscle developmental defects and cardiomyopathy, and diagnosis and treatment of hereditary sensory neuropathy type 1 and the sphingolipidoses. The present invention further relates to methods of screening

agents that modulate the expression and/or activity of polynucleotides and/or polypeptides involved in sphingolipid metabolism.

Description of the Related Art

Breast cancer is a significant health problem for women in the United States and throughout the world. Although advances have been made in detection and treatment of the disease, breast cancer remains the most common form of cancer, and the second leading cause of cancer death, in American women. Among African-American women and women between 15 and 54 years of age, breast cancer is the leading cause of cancer death. One out of every eight women in the United States will develop breast cancer, a risk which has increased 52% during 1950-1990. In 1994, it is estimated that 182,000 new cases of female breast cancer were diagnosed, and 46,000 women died from the disease.

No vaccine or other universally successful method for the prevention or treatment of breast cancer is currently available. Management of the disease currently relies on a combination of early diagnosis (through routine breast screening procedures) and aggressive treatment, which may include one or more of a variety of treatments such as surgery, radiotherapy, chemotherapy and hormone therapy. The course of treatment for a particular breast cancer is often selected based on a variety of prognostic parameters, including an analysis of specific tumor markers. However, the use of established markers often leads to a result that is difficult to interpret.

With current therapies, tumor invasiveness and metastasis is a critical determinant in the outcome for breast cancer patients. Although the five year survival for women diagnosed with localized breast cancer is about 90%, the five year survival drops to 18% for women whose disease has metastasized. Present therapies are inadequate for inhibiting tumor invasiveness for the large population of women with this severe disease.

Colon cancer is the second most frequently diagnosed malignancy in the United States as well as the second most common cause of cancer death. The five-year survival rate for patients with colorectal cancer detected in an early localized stage is 92%; unfortunately, only 37% of colorectal cancer is diagnosed at this stage. The survival rate drops to 64% if the cancer is allowed to spread to adjacent organs or lymph nodes, and to 7% in patients with distant metastases.

The prognosis of colon cancer is directly related to the degree of penetration of the tumor through the bowel wall and the presence or absence of nodal involvement, consequently, early detection and treatment are especially important. Currently, diagnosis is aided by the use of screening assays for fecal occult blood, sigmoidoscopy, colonoscopy and double contrast barium enemas. Treatment regimens are determined by the type and stage of the cancer, and include surgery, radiation therapy and/or chemotherapy. Recurrence following surgery (the most common form of therapy) is a major problem and is often the ultimate cause of death. In spite of considerable research into therapies for the disease, colon cancer remains difficult to diagnose and treat. In spite of considerable research into therapies for these and other cancers, colon cancer remains difficult to diagnose and treat effectively. Accordingly, improvements are needed in the treatment, diagnosis and prevention of breast and colon cancer. The present invention fulfills this need and further provides other related advantages.

Mutations that result in failure or dysregulation of sphingolipid synthesis or catabolism are directly responsible for a number of human diseases, including hereditary sensory neuropathy type 1 and the group of lysosomal storage diseases called the sphingolipidoses (Bejaoui, K., Wu, C., Scheffler, M. D., Haan, G., Ashby, P., Wu, L., de Jong, P. and Brown, R. H., Jr. (2001). *Nat Genet* 27, 261-2.; Dawkins, J. L., Hulme, D. J., Brahmbhatt, S. B., Auer-Grumbach, M. and Nicholson, G. A. (2001). *Nat Genet* 27, 309-12.; Gable, K., Han, G., Monaghan, E., Bacikova, D., Natarajan, M., Williams, R. and Dunn, T. M.

(2002). *J Biol Chem* 277, 10194-200.). A large body of evidence now indicates that sphingolipid metabolites and enzymes of sphingolipid metabolism play important roles in regulating cell migration, stress response, survival, differentiation, senescence, apoptosis, receptor signaling, and endocytosis in eukaryotic cells. These findings suggest molecular mechanisms by which sphingolipids may affect animal physiology and contribute to disease states.

Sphingosine-1-phosphate (**S-1-P**) is an endogenous sphingolipid metabolite present in most mammalian cells and in serum. Like other sphingolipid metabolites such as ceramide and sphingosine, S-1-P participates in specific signal transduction pathways. Many of the effects of S-1-P signaling, which include promotion of cellular proliferation, enhancement of migration, inhibition of apoptosis and stimulation of angiogenesis, influence the transformation, growth, drug resistance, vascularity and metastatic capacity of cancer cells. Several observations support the notion that sphingosine kinase (SK) and sphingosine-1-phosphate lyase (SPL) may be cancer related genes. First, the overexpression of SK in NIH3T3 fibroblasts leads to oncogenic transformation as determined by the ability of transfected cells to form foci *in vitro* and to form fibrosarcomas in NOD/SCID mice. Second, human SPL was cloned and mapped to 10q21, a chromosomal region frequently deleted in a variety of human cancers. Taken together, these observations raise the possibility that SK and SPL may be potentially effective targets for pharmacological intervention in the treatment of cancer. Accordingly, the present invention provides methods for screening agents that modulate sphingolipid metabolism. Further, the present invention provides methods for detecting and treating cancer.

Critical steps in the identification and development of new therapeutic agents are: (a) generation of candidate agents; and (b) screening of the candidate agents for efficacy and safety. With the advent of combinatorial chemistry protocols, large numbers of potential compounds, known as libraries, can be rapidly generated. Such libraries serve as collections of potential

therapeutic agents. Following generation of a library of potential therapeutic agents, the library must be screened to identity the promising candidates.

For screening purposes, a number of in vitro high throughput screening protocols have been developed. However, these in vitro screening assays must be followed by in vivo screening assays. Since it is undesirable to immediately screen compounds that show promise from in vitro assays in humans, an important step in the identification of therapeutic agents for such cellular proliferative diseases is the screening of potential therapeutic compounds in non-human animal models. As such, non-human animal models of cancer and other cellular proliferative diseases play an important role in the discovery of therapeutic agents for such diseases.

One type of non-human animal model that can be used for screening purposes to identify therapeutic agents for use in treating cancer and other cellular proliferative diseases is a non-human mammalian model, *e.g.* mice, *etc.* However, mice are expensive, have a slow reproduction time, and generate small numbers of offspring. As such, they are less than ideal for many high throughput screening assays.

Accordingly, there is a need for additional cellular and animal models for the identification of therapeutic agents for cancer and other diseases associated with altered sphingolipid metabolism. Of particular interest would be the development of a model in a biological system having a relatively short life cycle and a rapid growth cycle characterized by the production of large numbers of progeny.. Preferably, such a model system should also be relatively simple and economic to maintain.

BRIEF SUMMARY OF THE INVENTION

As noted above, the present invention relates generally to cancer detection and therapy. The invention is more particularly related to polynucleotides encoding polypeptides involved in the metabolism and/or signaling

of sphingolipids, polypeptides, and to agents that modulate the expression and/or activity of such polypeptides and/or the alter the levels of sphingolipid intermediates. Such agents may be used, for example, to diagnose and/or treat cancers such as breast, colon, uterus, stomach, ovary, lung, kidney and rectum cancer, the diagnosis and treatment of muscle developmental defects and cardiomyopathy, and diagnosis and treatment of hereditary sensory neuropathy type 1 and the sphingolipidoses. The present invention further relates to methods of screening agents that modulate the components and intermediates involved in sphingolipid metabolism and/or signaling.

It is an aspect of the present invention to provide a method for identifying an agent that modulates sphingolipid metabolism, comprising (a) culturing a homozygous null mutant *Drosophila melanogaster* in the absence and presence of a candidate agent under conditions and for a time sufficient to observe in the mutant *Drosophila melanogaster* an effect of the agent on a level of either (i) at least one sphingolipid intermediate, or (ii) activity of at least one component of a sphingolipid pathway, wherein the mutant *Drosophila melanogaster* comprises a P-element transposon insertion in a gene encoding a component of a sphingolipid pathway that results in at least one of an altered level of at least one sphingolipid intermediate and an altered activity level of at least one sphingolipid pathway component; and (b) comparing the level of either (i) the sphingolipid intermediate that is generated, or (ii) the activity of the sphingolipid pathway component, in the presence of the candidate agent to the level in the absence of the candidate agent, wherein an altered level indicates the agent modulates sphingolipid metabolism. In certain embodiments the altered level of a sphingolipid intermediate comprises an increase in $C_{14/16}$ long chain bases, and in certain other embodiments the altered level of a sphingolipid intermediate comprises an increase in $C_{14/16}$ phosphorylated long chain bases. In certain embodiments the gene encoding a component of a sphingolipid pathway comprises a polynucleotide sequence set forth in any one of SEQ ID NOS:15, 24

and 25. In certain embodiments the homozygous null mutant *Drosophila melanogaster* exhibits a flightless phenotype, and in certain other embodiments the homozygous null mutant *Drosophila melanogaster* comprises a tumor. In certain embodiments the homozygous null mutant *Drosophila melanogaster* comprises a T2 segment which comprises abnormal developmental patterning of thoracic muscles. In certain embodiments the altered level of the sphingolipid intermediate that is generated in the presence of the candidate agent comprises a decrease in sphingosine-1-phosphate and in certain embodiments the altered level of the sphingolipid intermediate that is generated in the presence of the candidate agent comprises an increase in sphingosine-1-phosphate.

In still other embodiments the altered level of the activity of the sphingolipid pathway component in the presence of the candidate agent comprises a decrease in sphingosine-1-phosphate lyase (SPL) activity, while in other embodiments the altered level of the activity of the sphingolipid pathway component in the presence of the candidate agent comprises an increase in sphingosine-1-phosphate lyase (SPL) activity. In still other embodiments the altered level of the activity of the sphingolipid pathway component in the presence of the candidate agent comprises a decrease in sphingosine kinase (SK) activity, while in other embodiments the altered level of the activity of the sphingolipid pathway component in the presence of the candidate agent comprises an increase in sphingosine kinase (SK) activity. In certain embodiments the agent inhibits SK activity, and in certain other embodiments the agent inhibits SPL activity. In certain embodiments the agent comprises a 1-aryl-2-dimethylaminopropane-1, 3-diol derivative, and in certain other embodiments the derivative comprises a substitution of a fatty acid amide group. In certain further embodiments the substitution comprises two N-methyl groups. In another embodiment the agent increases activity of serine palmitoyltransferase.

Turning to another aspect, the present invention provides a method for identifying an agent that modulates sphingolipid metabolism, comprising (a)

culturing a homozygous null mutant *Drosophila melanogaster* in the absence and presence of a candidate agent under conditions and for a time sufficient to observe in said mutant *Drosophila melanogaster* an effect of the agent on a level of either (i) at least one sphingolipid intermediate, or (ii) activity of at least one component of a sphingolipid pathway, wherein the mutant *Drosophila melanogaster* comprises a P-element transposon insertion in a gene encoding a component of a sphingolipid pathway that results in an altered activity level of at least one sphingolipid pathway component, and wherein the mutant *Drosophila melanogaster* exhibits a flightless phenotype that results from said insertion; and (b) comparing flight performance of the mutant *Drosophila* that is cultured in the presence of the candidate agent to the flight performance of the mutant *Drosophila* that is cultured in the absence of the candidate agent, wherein an increased flight performance of the mutant *Drosophila* cultured in the presence of the agent indicates the agent modulates sphingolipid metabolism. In certain embodiments the mutant *Drosophila melanogaster* comprises a homozygous mutation in a gene encoding a sphingosine-1-phosphate lyase (SPL), and in certain embodiments the homozygous null mutant *Drosophila melanogaster* comprises a T2 segment which comprises abnormal developmental patterning of thoracic muscles. In certain embodiments the agent that modulates sphingolipid metabolism inhibits sphingosine kinase activity.

In yet another embodiment there is provided a method for identifying an agent that modulates sphingolipid signaling, comprising (a) culturing a homozygous null mutant *Drosophila melanogaster* in the absence and presence of a candidate agent under conditions and for a time sufficient to observe in said mutant *Drosophila melanogaster* an effect of the agent on a level of at least one sphingolipid intermediate, wherein the mutant *Drosophila melanogaster* comprises a P-element transposon insertion in a gene encoding a component of a sphingolipid pathway that results in an altered level of at least one sphingolipid intermediate; and (b) comparing the level of the sphingolipid intermediate that is

generated in the presence of the candidate agent to the level in the absence of the candidate agent, wherein an altered level indicates the agent modulates sphingolipid signaling. It is also an aspect of the invention to provide an agent identified by the method of any one of the above described methods, which in certain embodiments is a composition comprising such agent in combination with a physiologically acceptable excipient. In certain embodiments there is provided a composition comprising an agent that increases flight performance in a homozygous null mutant *Drosophila melanogaster*, wherein the mutant *Drosophila melanogaster* comprises a P-element transposon insertion in a gene encoding a sphingosine-1-phosphate lyase (SPL) polypeptide that comprises the amino acid sequence set forth in SEQ ID NO:16, and wherein the mutant *Drosophila melanogaster* exhibits a flightless phenotype that results from said insertion, and in certain further embodiments the agent inhibits sphingosine kinase activity.

According to certain other embodiments of the present invention there is provided a method for preparing a sphingosine-1-phosphate lyase (SPL) polypeptide, comprising culturing a host cell transformed or transfected with a nucleic acid construct comprising a promoter operably linked to a polynucleotide comprising the nucleotide sequence set forth in SEQ ID NO:15; and recovering a sphingosine-1-phosphate lyase polypeptide.

In still other embodiments there is provided a method for identifying an agent that modulates sphingosine-1-phosphate lyase activity, comprising (a) contacting a candidate agent with an isolated polypeptide that comprises an amino acid sequence selected from an amino acid sequence set forth in SEQ ID NO:16 and an amino acid sequence having at least 90% identity to the sequence set forth in SEQ ID NO:16, wherein the polypeptide has sphingosine-1-phosphate lyase activity, and wherein the step of contacting is carried out under conditions and for a time sufficient to allow the candidate agent to interact with said polypeptide; and (b) determining degradation by the polypeptide of sphingosine-1-phosphate or a sphingosine-1-phosphate derivative thereof in the presence of the candidate

agent, relative to degradation by said polypeptide of sphingosine-1-phosphate or a sphingosine-1-phosphate derivative thereof in the absence of the candidate agent, and therefrom identifying an agent that modulates sphingosine-1-phosphate lyase activity.

In another embodiment there is provided a method for identifying an agent that modulates sphingosine-1-phosphate lyase activity, comprising (a) contacting a candidate agent with a biological sample that comprises a cell which expresses a polypeptide that comprises an amino acid sequence selected from an amino acid sequence set forth in SEQ ID NO:16 and an amino acid sequence having at least 90% identity to the sequence set forth in SEQ ID NO:16, wherein said polypeptide has sphingosine-1-phosphate lyase activity, and wherein the step of contacting is carried out under conditions and for a time sufficient to allow the candidate agent to interact with the polypeptide; and (b) determining degradation by said polypeptide of sphingosine-1-phosphate or a sphingosine-1-phosphate derivative thereof in the presence of the candidate agent, relative to degradation by said polypeptide of sphingosine-1-phosphate or a sphingosine-1-phosphate derivative thereof in the absence of the candidate agent, and therefrom identifying an agent that modulates sphingosine-1-phosphate lyase activity. In certain embodiments the step of determining comprises an *in vitro* assay of an extract from the cell.

In certain embodiments the invention provides a composition comprising an agent that modulates sphingosine-1-phosphate lyase activity of a polypeptide, said polypeptide comprising a sequence set forth in SEQ ID NO:16, in combination with a pharmaceutically acceptable carrier. In certain further embodiments the agent comprises a polynucleotide. In certain other further embodiments the agent comprises an antibody or an antigen-binding fragment thereof that specifically binds a sphingosine phosphate lyase (SPL) polypeptide comprising the sequence set forth in SEQ ID NO:16, and wherein the antibody increases the ability of the SPL polypeptide to degrade sphingosine-1-phosphate.

In certain embodiments the invention provides a method for inhibiting growth of a cancer cell, comprising contacting the cancer cell with an agent that increases sphingosine-1-phosphate lyase activity of a polypeptide comprising a sequence set forth in SEQ ID NO:16. In certain further embodiments the agent increases expression of an endogenous sphingosine-1-phosphate lyase gene, and in certain other further embodiments the cancer cell is a breast cancer cell.

According to another embodiment there is provided a method for inhibiting development of cancer, metastasis, or both development of cancer and metastasis in a mammal, comprising administering to said mammal an agent that increases sphingosine-1-phosphate lyase activity of a polypeptide comprising a sequence set forth in SEQ ID NO:16. In certain further embodiments the agent increases expression of an endogenous sphingosine-1-phosphate lyase gene, and in certain still further embodiments the agent is linked to a targeting component, which in certain still further embodiments is an anti-tumor antibody and in certain other still further embodiments binds to an estrogen receptor. In certain embodiments the mammal is afflicted with breast cancer.

It is another aspect of the present invention to provide a method for determining the presence of cancer in a patient, comprising the steps of (a) contacting a first biological sample comprising at least one polynucleotide and being obtained from a patient suspected of having cancer with at least one oligonucleotide that is specific for a polynucleotide which comprises a nucleic acid sequence as set forth in SEQ ID NO:23; (b) detecting an amount of the olignucleotide that hybridizes to the polynucleotide in the first sample; and (d) comparing the amount of oligonucleotide that hybridizes to the polynucleotide in the first sample to an amount of oligonucleotide that hybridizes to a polynucleotide in a second biological sample obtained from a normal control subject known to be free of cancer, wherein a statistically significant decrease in the amount of olignucleotide that hybridizes to the polynucleotide in the first biological sample

relative to the amount of oligonucleotide that hybridizes to the polynucleotide in the second sample signifies the presence of a cancer in said patient.

It is another aspect of the present invention to provide a method for diagnosing a disease associated with altered sphingolipid metabolism comprising (a) contacting a first biological sample comprising at least one polynucleotide and being obtained from a patient suspected of having a disease associated with altered sphingolipid metabolism with at least one oligonucleotide that is specific for a polynucleotide which comprises a nucleic acid sequence as set forth in SEQ ID NO:23; (b) detecting an amount of the olignucleotide that hybridizes to the polynucleotide in the first sample; and (d) comparing the amount of oligonucleotide that hybridizes to the polynucleotide in the first sample to an amount of oligonucleotide that hybridizes to a polynucleotide in a second biological sample obtained from a normal control subject known to be free of a disease associated with altered sphingolipid metabolism, wherein a statistically significant decrease in the amount of olignucleotide that hybridizes to the polynucleotide in the first biological sample relative to the amount of oligonucleotide that hybridizes to the polynucleotide in the second sample signifies the presence of a disease associated with altered sphingolipid metabolism in said patient.

It is another aspect of the present invention to provide a method for determining the presence of a cancer in a patient, comprising the steps of (a) contacting a first biological sample comprising at least one polynucleotide and being obtained from a patient suspected of having cancer with at least one oligonucleotide that is specific for a polynucleotide which comprises a nucleic acid sequence as set forth in SEQ ID NO:22; (b) detecting an amount of the olignucleotide that hybridizes to the polynucleotide in the first sample; and (d) comparing the amount of oligonucleotide that hybridizes to the polynucleotide in the first sample to an amount of oligonucleotide that hybridizes to a polynucleotide in a second biological sample obtained from a normal control subject known to be free of cancer, wherein a statistically significant increase in the amount of

olignucleotide that hybridizes to the polynucleotide in the first biological sample relative to the amount of oligonucleotide that hybridizes to the polynucleotide in the second sample signifies the presence of a cancer in said patient.

It is another aspect of the present invention to provide a method for diagnosing a disease associated with altered sphingolipid metabolism comprising (a) contacting a first biological sample comprising at least one polynucleotide and being obtained from a patient suspected of having a disease associated with altered sphingolipid metabolism with at least one oligonucleotide that is specific for a polynucleotide which comprises a nucleic acid sequence as set forth in SEQ ID NO:22; (b) detecting an amount of the olignucleotide that hybridizes to the polynucleotide in the first sample; and (d) comparing the amount of oligonucleotide that hybridizes to the polynucleotide in the first sample to an amount of oligonucleotide that hybridizes to a polynucleotide in a second biological sample obtained from a normal control subject known to be free of a disease associated with altered sphingolipid metabolism, wherein a statistically significant increase in the amount of olignucleotide that hybridizes to the polynucleotide in the first biological sample relative to the amount of oligonucleotide that hybridizes to the polynucleotide in the second sample signifies the presence of a disease associated with altered sphingolipid metabolism in said patient. It is another aspect of the present invention to provide a method for treating a disease associated with altered sphingolipid metabolism in a patient, comprising administering to said patient an agent identified according to any of the above described methods. In certain further embodiments the disease is colon cancer, breast cancer, uterine cancer, stomach cancer, ovarian cancer, lung cancer, kidney cancer, adenocarcinoma of the rectum, hereditary sensory neuropathy type 1, or any one of the sphingolipidoses.

Another embodiment of the present invention provides a method for identifying an agent that modulates sphingolipid metabolism, comprisingculturing a mutant yeast strain with sphingosine in the absence and presence of a candidate

agent under conditions and for a time sufficient to observe in said mutant yeast strain an altered level of either (i) at least one sphingolipid intermediate, or (ii) activity of at least one component of a sphingolipid pathway, wherein the mutant yeast strain comprises a null allele of at least one gene encoding a component of a sphingolipid pathway that results in an altered activity level of at least one sphingolipid pathway component, and wherein said mutant strain of yeast has been genetically altered to express at least one nonendogenous sphingolipid pathway component and wherein the mutant yeast strain exhibits growth inhibition in the presence of sphingosine; and comparing growth of the mutant yeast strain in the presence of the candidate agent to the growth of the mutant yeast strain in the absence of the candidate agent, wherein an increase in growth of the mutant yeast strain in the presence of the agent indicates the agent modulates sphingolipid metabolism. In one embodiment, the at least one gene comprises DPL1. In another embodiment the at least one gene comprises DPL1 and LCB4. In another embodiment, the nonendogenous sphingolipid pathway component comprises human SPHK1. In certain embodiments, the altered level of the sphingolipid intermediate in the presence of the candidate agent comprises a decrease in at least one LCBP. In one embodiment, the LCBP comprises sphingosine-1-phosphate. In another embodiment, the altered level of the activity of the sphingolipid pathway component in the presence of the candidate agent comprises a decrease in the human SPHK1 activity.

In certain embodiments, the present invention provides a method for identifying an inhibitor of SK, comprising culturing a null mutant yeast strain with sphingosine in the absence and presence of a candidate agent under conditions and for a time sufficient to observe in said mutant yeast strain an altered ability of said yeast mutant strain to grow, wherein the mutant yeast strain comprises a null allele of at least DPL1 and LCB4, and wherein said mutant strain of yeast has been genetically altered to express nonendogenous SK and wherein the mutant yeast strain exhibits growth inhibition in the presence of sphingosine; and

comparing growth of the mutant yeast strain in the presence of the candidate agent to the growth of the mutant yeast strain in the absence of the candidate agent, wherein an increase in growth of said mutant yeast strain in the presence of the agent indicates the agent is an inhibitor of SK.

In certain embodiments, the present invention provides a method for identifying an inhibitor of SK, comprising culturing a null mutant yeast strain with an inducer in the absence and presence of a candidate agent under conditions and for a time sufficient to observe altered growth in said mutant yeast strain, wherein the mutant yeast strain comprises a null allele of at least DPL1, LCB4, and SPP, and wherein said mutant strain of yeast has been genetically altered to express nonendogenous SK under the control of a promoter that is induced by the inducer and wherein the mutant yeast strain exhibits growth inhibition in the presence of the inducer; and comparing growth of the mutant yeast strain in the presence of the candidate agent to the growth of the mutant yeast strain in the absence of the candidate agent, wherein an increase in growth of said mutant yeast strain in the presence of the candidate agent indicates the candidate agent is an inhibitor of SK. In one embodiment, the inducible promoter is a galactose-inducible promoter. In certain embodiment, the inducer includes but is not limited to galactose.

The present invention also provides a method for identifying an agent that modulates sphingolipid metabolism, comprising culturing a mutant yeast strain with sphingosine in the absence and presence of a candidate agent under conditions and for a time sufficient to observe in said mutant yeast strain an altered level of either (i) at least one sphingolipid intermediate, or (ii) activity of at least one component of a sphingolipid pathway, wherein the mutant yeast strain comprises a null allele of at least one gene encoding a component of a sphingolipid pathway that results in an altered activity level of at least one sphingolipid pathway component, and wherein said mutant strain of yeast has been genetically altered to express at least one nonendogenous sphingolipid

pathway component and wherein the mutant yeast strain exhibits growth inhibition in the presence of sphingosine; and comparing the level of either (i) or (ii) in the mutant yeast strain cultured in the presence of the candidate agent to the level of either (i) or (ii) in the mutant yeast strain cultured in the absence of the candidate agent, wherein an altered level in the presence of the agent indicates the agent modulates sphingolipid metabolism. In one embodiment, the altered level of said at least one sphingolipid intermediate comprises a decrease in S-1-P. In certain embodiments, the altered level of said activity of at least one component of a sphingolipid pathway comprises a decrease in the activity of said at least one nonendogenous sphingolipid pathway component. In one embodiment, the nonendogenous sphingolipid pathway component comprises human SPHK1.

In another embodiment, the present invention provides a method for identifying an agent that modulates sphingolipid metabolism, comprising culturing a null mutant yeast strain with sphingosine in the absence and presence of a candidate agent under conditions and for a time sufficient to observe altered growth of said mutant yeast strain, wherein the mutant yeast strain comprises a null allele of at least one gene encoding a component of a sphingolipid pathway that results in an altered activity level of at least one sphingolipid pathway component, and wherein said mutant strain of yeast has been genetically altered to express at least one nonendogenous sphingolipid pathway component, and wherein the mutant yeast strain exhibits growth inhibition in the presence of sphingosine; and comparing growth of the mutant yeast strain in the presence of the candidate agent to growth of the mutant yeast strain in the absence of the candidate agent, wherein an increase in growth of said mutant yeast strain in the presence of the candidate agent indicates the agent modulates sphingolipid metabolism. In one embodiment the null allele of at least one gene encoding a component of a sphingolipid pathway comprises DPL1. In another embodiment, the at least one gene comprises DPL1 and LCB4. In certain embodiments, the at

least one nonendogenous sphingolipid pathway component comprises human SPHK1.

The present invention also provides a method for identifying an agent that modulates sphingolipid metabolism, comprising culturing a mutant yeast strain with an inducer in the absence and presence of a candidate agent under conditions and for a time sufficient to observe in said mutant yeast strain an altered level of either (i) at least one sphingolipid intermediate, or (ii) activity of at least one component of a sphingolipid pathway, wherein the mutant yeast strain comprises a null allele of at least one gene encoding a component of a sphingolipid pathway that results in an altered activity level of at least one sphingolipid pathway component, and wherein said mutant strain of yeast has been genetically altered to express at least one nonendogenous sphingolipid pathway component under the control of a promoter that is induced by the inducer and wherein the mutant yeast strain exhibits growth inhibition in the presence of the inducer; and comparing the level of either (i) or (ii) in the mutant yeast strain cultured in the presence of the candidate agent to the level of either (i) or (ii) in the mutant yeast strain cultured in the absence of the candidate agent, wherein an altered level in the presence of the agent indicates the agent modulates sphingolipid metabolism. In certain embodiments, the altered level of said at least one sphingolipid intermediate comprises a decrease in LCBPs. In another embodiment the altered level of said activity of at least one component of a sphingolipid pathway comprises a decrease in the activity of said at least one nonendogenous sphingolipid pathway component. In yet another embodiment, the at least one nonendogenous sphingolipid pathway component comprises human SPHK1. In certain embodiments the at least one gene comprises DPL1. In another embodiment, the at least one gene comprises DPL1 and LCB4. In yet another embodiment, the at least one gene comprises DPL1, LCB4, and YSR2.

The present invention also provides a method for identifying an agent that modulates sphingolipid metabolism, comprising culturing a null mutant

yeast strain with an inducer in the absence and presence of a candidate agent under conditions and for a time sufficient to observe altered growth of said mutant yeast strain, wherein the mutant yeast strain comprises a null allele of at least one gene encoding a component of a sphingolipid pathway that results in an altered activity level of at least one sphingolipid pathway component, and wherein said mutant strain of yeast has been genetically altered to express at least one nonendogenous sphingolipid pathway component under the control of a promoter that is induced by the inducer and wherein the mutant yeast strain exhibits growth inhibition in the presence of the inducer; and comparing growth of the mutant yeast strain in the presence of the candidate agent to growth of the mutant yeast strain in the absence of the candidate agent, wherein an increase in growth of said mutant yeast strain in the presence of the candidate agent indicates the agent modulates sphingolipid metabolism. In one embodiment, the at least one gene comprises DPL1. In another embodiment, the at least one gene comprises DPL1 and LCB4. In yet another embodiment, the at least one gene comprises DPL1, LCB4, and YSR2. In certain embodiments, the at least one nonendogenous sphingolipid pathway component comprises human SPHK1.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references (including websites) disclosed herein are hereby incorporated by reference in their entireties as if each was incorporated individually.

BRIEF DESCRIPTION OF THE FIGURES AND SEQUENCE IDENTIFIERS

Figure 1 shows the amino acid sequence of 2 potential *Drosophila melanogaster* SK proteins aligned with the amino acid sequence of a human SK protein. (DSK1747 set forth in SEQ ID NO:19; DSK2159 set forth in SEQ ID NO:20).

Figure 2 shows a first chemical synthesis scheme.

Figure 3 shows a second chemical synthesis scheme.

Figure 4 is a schematic diagram showing a first yeast screen for inhibitors of SK.

Figure 5 is a schematic diagram showing a second yeast screen for inhibitors of SK.

SEQ ID NO:1 is the determined cDNA sequence of S. cerevisiae SPL

SEQ ID NO:2 is the amino acid sequence of S. cerevisiae SPL encoded by the polynucleotide sequence set forth in SEQ ID NO:1

SEQ ID NO:3 is the determined cDNA sequence of *C. elegans* SPL

SEQ ID NO:4 is the amino acid sequence of *C. elegans* SPL encoded by the polynucleotide sequence set forth in SEQ ID NO:3

SEQ ID NO:5 is the determined cDNA sequence of the mouse SPL

SEQ ID NO:6 is the amino acid sequence of mouse SPL encoded by the polynucleotide sequence set forth in SEQ ID NO:5

SEQ ID NO:7 is the determined cDNA sequence of the full-length human SPL

SEQ ID NO:8 is the amino acid sequence of human SPL encoded by the polynucleotide sequence set forth in SEQ ID NO:7

SEQ ID NO:9 is the determined cDNA sequence of a human SPL with a deletion

SEQ ID NO:10 is the amino acid sequence of a human SPL with a deletion, encoded by the polynucleotide sequence set forth in SEQ ID NO:9.

SEQ ID NO:11 is the amino acid sequence of *C. elegans* SPL encoded by the polynucleotide sequence set forth in SEQ ID NO:12

SEQ ID NO:12 is the determined cDNA sequence of a *C. elegans* SPL

SEQ ID NO:13 is a PCR primer

SEQ ID NO:14 is a PCR primer

SEQ ID NO:15 is the determined cDNA sequence encoding the *Drosophila melanogaster* SPL

SEQ ID NO:16 is the amino acid sequence of the *Drosophila melanogaster* SPL, encoded by the cDNA sequence set forth in SEQ ID NO:15

SEQ ID NO:17 is the determined cDNA sequence of a human SPL as set forth in Genbank Accession No: AF144638.

SEQ ID NO:18 is the amino acid sequence of a human SPL encoded by the polynucleotide sequence provided in SEQ ID NO:17.

SEQ ID NO:19 is the amino acid sequence of a first *Drosophila melanogaster* SK protein.

SEQ ID NO:20 is the amino acid sequence of a second *Drosophila melanogaster* SK protein.

SEQ ID NO:21 is the amino acid sequence of a human SK protein.

SEQ ID NO:22 is the cDNA encoding the human SK protein set forth in SEQ ID NO:21.

SEQ ID NO:23 is a cDNA sequence of human SPL, encoding the amino acid sequence set forth in SEQ ID NO:18.

SEQ ID NO:24 is the full length cDNA sequence for a first *Drosophila melanogaster* SK1, GI:21429173, encoding the amino acid sequence set forth in SEQ ID NO:19 and 28.

SEQ ID NO:25 is the full length cDNA sequence for a second *Drosophila melanogaster* SK2, GI:17862169, encoding the amino acid sequence set forth in SEQ ID NO:20 and 29.

SEQ ID NO:26 is the full length cDNA sequence for *Drosophila melanogaster* SPL, clone GH13783, GI:15292460.

SEQ ID NO:27 is the full length cDNA sequence for *Drosophila melanogaster* SPL, clone LP04413, GI:15292460.

SEQ ID NO:28 is the full length amino acid sequence of *Drosophila melanogaster* SK1 CG1747.

SEQ ID NO:29 is the full length amino acid sequence of *Drosophila melanogaster* CG2159.

SEQ ID NO:30 is the polynucleotide coding region for the *Saccharomyces cerevisiaie* LCB4 protein as available from yeastgenome.org.

SEQ ID NO:31 is the amino acid sequence of the protein encoded by the polynucleotide of SEQ ID NO:30, the yeast LCB4 protein.

SEQ ID NO:32 is the polynucleotide coding region for the *Saccharomyces cerevisiaie* LCB5 protein as available from yeastgenome.org.

SEQ ID NO:33 is the amino acid sequence of the protein encoded by the polynucleotide of SEQ ID NO:32, the yeast LCB5 protein.

SEQ ID NO:34 is the polynucleotide coding region for the *Saccharomyces cerevisiaie* YSR2 protein (also referred to as LCB3) as available from yeastgenome.org.

SEQ ID NO:35 is the amino acid sequence of the protein encoded by the polynucleotide of SEQ ID NO:34, the yeast YSR2 protein (also referred to as LCB3).

SEQ ID NO:36 is the polynucleotide coding region for the *Saccharomyces cerevisiaie* YSR3 protein as available from yeastgenome.org.

SEQ ID NO:37 is the amino acid sequence of the protein encoded by the polynucleotide of SEQ ID NO:36, the yeast YSR3 protein.

SEQ ID NO:38 is the polynucleotide coding region for the *Saccharomyces cerevisiaie* SUR2 protein as available from yeastgenome.org.

SEQ ID NO:39 is the amino acid sequence of the protein encoded by the polynucleotide of SEQ ID NO:38, the yeast SUR2 protein.

SEQ ID NO:40 is a PCR primer as described in Example 17.

SEQ ID NO:41 is a PCR primer as described in Example 17.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides compositions and methods, including screening assays, for agents that modulate sphingolipid metabolism and/or signaling wherein the agents have an effect on a level of sphingolipid intermediates and/or the activity of one or more components of a sphingolipid metabolic and/or signaling pathway and further provides methods for screening for said agents. Agents of the present invention have utility in the detection, diagnosis, and therapy of cancer and other diseases associated with altered sphingolipid metabolism and/or signaling.

Generally, the present invention relates to involvement of sphingolipid intermediates, and components involved in sphingolipid metabolism and/or signaling pathways, in numerous human diseases, including a variety of cancers (*e.g.* colon, breast, uterus, stomach, ovary, lung, kidney and adenocarcinoma of the rectum). In particular, the present invention derives from the unexpected observation that SPL expression is reduced in colloid cancer of the colon and adenocarcinoma of the colon. Also according to the present invention as disclosed below in greater detail, reduced SPL expression is observed in adenocarcinoma of the uterus, and SK expression is increased in a variety of tumor tissues as compared to normal tissue (*e.g.* breast, uterus, stomach, ovary, lung, kidney and adenocarcinoma of the rectum). Other components involved in sphingolipid metabolism and/or signaling pathways are also associated with other human diseases. In particular, failure and/or dysregulation of sphingolipid synthesis and/or catabolism are directly responsible for a number of human diseases, including hereditary sensory neuropathy type 1 and the group of lysosomal storage diseases called the sphingolipidoses (Bejaoui, K., Wu, C., Scheffler, M. D., Haan, G., Ashby, P., Wu, L., de Jong, P. and Brown, R. H., Jr. (2001). *Nat Genet* 27, 261-2.; Dawkins, J. L., Hulme, D. J., Brahmbhatt, S. B., Auer-Grumbach, M. and Nicholson, G. A. (2001). *Nat Genet* 27, 309-12.;

Gable, K., Han, G., Monaghan, E., Bacikova, D., Natarajan, M., Williams, R. and Dunn, T. M. (2002). *J Biol Chem* 277, 10194-200.).

The present invention further relates in certain embodiments to the unanticipated observation that *Drosophila melanogaster* SPL and SK mutants demonstrate altered sphingolipid metabolism. Surprisingly, SPL mutant flies have a flightless phenotype that can be restored by growing such mutant flies in the presence of an agent that modifies a component of the sphingolipid metabolic and/or signaling pathway. Thus, the present invention provides mutant and/or transgenic *Drosophila melanogaster* that have altered sphinoglipid metabolism and/or signaling that can be used to screen agents useful for the detection, diagnosis, and treatment of the human diseases described herein.

In certain other embodiments, the present invention relates to the surprising discovery that components of yeast and mammalian sphingolipid pathways can be functionally combined in a yeast mutant expression system. Unexpectedly, such yeast systems exhibit cell growth inhibition in response to elevated intracellular phosphorylated long chain sphingoid bases (LCBP) (*e.g.*, S-1-P), unlike many mammalian cells that proliferate in response to excessive accumulations of LCBPs. These and related embodiments advantageously provide mutant and/or recombinant yeast strains having sphingolipid pathway defects that permit the use of such strains as indicator cells in screening assays for agents which modulate sphingolipid metabolism, and in particular, for SK inhibitors.

<u>Components of Sphingolipid Metabolism and/or Signaling</u>

Any component of the sphingolipid metabolic and/or signaling pathway may be regarded as within the context of the present invention. As such, components of the sphingolipid metabolic and/or signaling pathway include but are not limited to, enzymes involved in these pathways (and the polynucleotides encoding said enzymes), such as, SPL, SK, ceramidase, S-1-PP, serine

palmitoyltransferase (SPT), 3-keto dihydrosphingosine reductase, ceramide synthase, sphingosine desaturase, ceramide kinase, phosphoethanolamine cytidylyltransferase, CDP-ethanolamine phosphotransferase, acid sphingomyelinase, sphingomyelin synthase, neutral sphingomyelinase, oxosphinanine reductase, and glucosylceramide synthase. Components of the sphingolipid metabolic and/or signaling pathway further include intracellular or cell surface receptors, and the polynucleotides encoding said receptors, such as EDG receptors (*e.g.* EDG1, EDG3, EDG5, EDG6, EDG8) and CFTR.

Generally sphingolipid metabolism can be viewed as all synthetic and catabolic pathways involving any sphingolipid or sphingolipid intermediate as described herein. Sphingolipid signaling pathways are known in the art and can generally be viewed herein as any signaling pathway activated by a sphingolipid, such as the signaling pathways of sphingosine-1-phosphate such as those described in Pyne, S., and N.J. Pyne. 2000 *Biochem. J.* 349:385-402 and Pyne, S., and N.J. Pyne, 2000 *Pharmacology and Therapeutics* 88:115-131. However, the skilled artisan would recognize that other sphingolipid signaling pathways fall within the scope of the present invention and are contemplated herein.

The present invention therefore provides polypeptides involved in sphingolipid metabolism and/or signaling, and polynucleotides encoding such polypeptides. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length endogenous (*i.e.,* native) proteins and variants of endogenous sequences that are involved in sphingolipid metabolism and/or signaling. Illustrative polypeptides of the present invention are set forth in SEQ ID NOs:2, 4, 6, 8, 10, 11, 16, 18-21, and 28-29. Particularly illustrative polypeptides are set forth in SEQ ID NOs:16, 18-21, and 28-29. "Variants" are polypeptides that differ in sequence from the polypeptides of the present invention only in substitutions, deletions and/or other modifications, such that the variant retains ability to modulate sphingolipid metabolism and/or signaling, for example by effecting the levels of one or more sphingolipid intermediates, such as

intracellular S-1-P, ceramide, sphingosine, or other LCB or LCBP levels, which may be determined using a representative method described herein. Polypeptide variants generally encompassed by the present invention will typically exhibit at least about 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or more identity along its length, to a polypeptide sequence set forth herein. Within a polypeptide variant, amino acid substitutions are preferably made at no more than 50% of the amino acid residues in the native polypeptide, and more preferably at no more than 25% of the amino acid residues. Such substitutions are preferably conservative. A conservative substitution is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. In general, the following amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. Substitutions, deletions and/or amino acid additions may be made at any location(s) in the polypeptide, provided that the modification does not diminish the ability of the variant to modulate intracellular S-1-P levels. Thus, a variant may comprise only a portion of a native polypeptide sequence as provided herein. In addition, or alternatively, variants may contain additional amino acid sequences (such as, for example, linkers, tags and/or ligands), preferably at the amino and/or carboxy termini. Such sequences may be used, for example, to facilitate purification, detection or cellular uptake of the polypeptide.

When comparing polypeptide sequences, two sequences are said to be "identical" if the sequence of amino acids in the two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20

contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenes pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS 5*:151-153; Myers, E.W. and Muller W. (1988) *CABIOS 4*:11-17; Robinson, E.D. (1971) *Comb. Theor 11*:105; Saitou, N. Nei, M. (1987) *Mol. Biol. Evol. 4*:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad., Sci. USA 80*:726-730.

Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nucl. Acids Res.*

25:3389-3402 and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent sequence identity for the polynucleotides and polypeptides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. For amino acid sequences, a scoring matrix can be used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment.

An "isolated" polypeptide is one that is removed from its original environment. For example, a naturally-occurring protein or polypeptide is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are also purified, *e.g.*, are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure.

In one embodiment of the present invention, a polypeptide comprises a fusion protein comprising a component of a sphingolipid metabolic and/or signaling pathway. The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins, typically in the form of pharmaceutical compositions, *e.g.*, vaccine compositions, comprising a physiologically acceptable carrier or excipient. The fusion proteins may comprise multiple polypeptides or portions/variants thereof, as described herein, and may further comprise one or more polypeptide segments for facilitating the expression, purification, detection, and/or activity of the polypeptide(s).

In general, polypeptide components of a sphingolipid metabolic and/or signaling pathway, and polynucleotides encoding such polypeptides as described herein, may be prepared using any of a variety of techniques that are well known in the art. For example, a DNA sequence encoding native SK, SPL or SPT may be prepared by amplification from a suitable cDNA or genomic library using, for example, polymerase chain reaction (PCR) or hybridization techniques. Libraries may generally be prepared and screened using methods well known to those of ordinary skill in the art, such as those described in Sambrook et al., *Molecular Cloning: A Laboratory Manual,* Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989. cDNA libraries may be prepared from any of a variety of sources known to contain enzymes involved in sphingolipid metabolism. For example, SPL activity is ubiquitous with regard to species and mammalian tissues, with the exception of platelets, in which SPL activity is notably absent. In rat tissues, the highest levels of activity have been demonstrated in intestinal mucosa, liver and Harderian gland, with low activity in skeletal muscle and heart. Activity has also been demonstrated in a number of human (hepatoma cell line HB 8065, cervical carcinoma HeLa), mouse (hepatoma line BW1, mouse embryo 3T3-L1, Swiss 3T3 cells) and other cell lines, as well as in human cultured fibroblasts. Preferred cDNA libraries may prepared from human liver, intestine or brain tissues or cells. Other libraries that may be employed will be apparent to those of ordinary skill in the art. Primers for use in amplification may be readily designed based on the polynucleotide sequence of a native SPL, SK, SPT, S-1-PP or other polynucleotide as provided herein or known to the skilled artisan and available on any number of public databases.

A polynucleotide encoding a polypeptide component involved in a sphingolipid pathway (metabolic and/or signaling), such as a polynucleotide encoding SPL, SK, SPT, and S-1-PP, are also provided by the present invention. A polynucleotide as used herein may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA

molecules. Thus, within the context of the present invention, a polynucleotide encoding a polypeptide may also be a gene. A gene is a segment of DNA involved in producing a polypeptide chain; it includes regions preceding and following the coding region (leader and trailer) as well as intervening sequences (introns) between individual coding segments (exons). Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials. "Isolated," as used herein, means that a polynucleotide is substantially away from other coding sequences, and that the DNA molecule does not contain large portions of unrelated coding DNA, such as large chromosomal fragments or other functional genes or polypeptide coding regions. Of course, this refers to the DNA molecule as originally isolated, and does not exclude genes or coding regions later added to the segment by the hand of man.

Polynucleotides of the present invention may comprise a native sequence (*i.e.,* an endogenous polynucleotide, for instance, a native or non-artificially engineered or naturally occurring gene as provided herein) encoding SPL, SK, SPT, or other components of the sphingolipid metabolic or signaling pathways, alternate form sequence, or a portion or splice variant thereof) or may comprise a variant of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the activity of the encoded polypeptide is not substantially diminished, as described herein. The effect on the activity of the encoded polypeptide may generally be assessed as described herein. Variants preferably exhibit at least about 70% identity, more preferably at least about 80%, 85%, 86%, 87%, 88%, 89%, identity and most preferably at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to a polynucleotide sequence that encodes a native polypeptide involved in sphingolipid metabolism or signaling, such as the polynucleotides set forth in SEQ ID NOs:1, 3, 5, 7, 9, 12, 15, 17, and 22-27 or an alternate form or a

portion thereof, and the polynucleotides that encode a polypeptide sequence as recited in any one of SEQ ID NOs:2, 4, 6, 8, 10, 11, 16, and 18-21, or a portion thereof. Particularly illustrative polynucleotides of the present invention comprise polynucleotides encoding a polypeptide comprising an amino acid sequence shown in Figure 1, such as the amino acid sequences set forth in SEQ ID NOs:18-21 and 28-29. The percent identity may be readily determined by comparing sequences using computer algorithms well known to those having ordinary skill in the art and described herein.

Polynucleotides that are substantially homologous to a sequence complementary to a polynucleotide as described herein are also within the scope of the present invention. "Substantial homology," as used herein refers to polynucleotides that are capable of hybridizing under moderately stringent conditions to a polynucleotide complementary to an SK, SPL, SPT, S-1-PP or other polynucleotide sequence provided herein, provided that the encoded polypeptide variant retains enzymatic or signaling activity. Suitable moderately stringent conditions include prewashing in a solution of 5X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50-65°C, 5X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS. Nucleotide sequences that, because of code degeneracy, encode a polypeptide encoded by any of the above sequences are also encompassed by the present invention.

A polynucleotide as described herein may be identified using standard yeast genetics known to the skilled artisan. A cDNA expression library may be generated using a regulatable yeast expression vector (*e.g.,* pYES, which is available from Invitrogen, Inc.) and standard techniques. A yeast mutant strain may then be transformed with the cDNA library, and endogenous cDNAs having the ability to functionally complement the yeast sphingolipid metabolism defect (*i.e.,* restore the ability to grow in the presence of D-*erythro*-sphingosine or other appropriate sphingolipid intermediate) may be isolated.

A polynucleotide encoding a polypeptide affecting sphingolipid metabolism and/or signaling may also be identified based on cross-reactivity of the protein product with antibodies that react to SPL, SK, SPT, and other polypeptides involved in sphingolipid metabolism or signaling, which may be prepared as described herein. Such screens may generally be performed using standard techniques (*see* Huynh et al., "Construction and Screening cDNA Libraries in λgt11," *in* D.M. Glover, ed., *DNA Cloning: A Practical Approach*, 1:49-78, 1984 (IRL Press, Oxford)).

Polypeptides of the present invention may be prepared by expression of recombinant DNA encoding the polypeptide in cultured host cells. Preferably, the host cells are bacteria, yeast, insect or mammalian cells, and preferably the host cells are *S. cerevisiae bst1Δ* cells. The recombinant DNA may be cloned into any expression vector suitable for use within the host cell and transfected into the host cell using techniques well known to those of ordinary skill in the art. A suitable expression vector contains a promoter sequence that is active in the host cell. A tissue-specific or conditionally active promoter may also be used. Preferred promoters express the polypeptide at high levels. As is readily appreciated by the skilled artisan, the polynucleotide encoding the polypeptide of interest is cloned into the expression vector such that it is operably linked to the promoter such that the polypeptide of interest is properly translated. Thus, in certain embodiments, the ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are generally located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Optionally, the construct may contain an enhancer, a transcription terminator, a poly(A) signal sequence, a bacterial or mammalian origin of replication and/or a selectable marker, all of which are well known in the art.

Enhancer sequences may be included as part of the promoter region or separately. Transcription terminators are sequences that stop RNA polymerase-mediated transcription. The poly(A) signal may be contained within the termination sequence or incorporated separately. A selectable marker includes any gene that confers a phenotype on the host cell that allows transformed cells to be identified. Such markers may confer a growth advantage under specified conditions. Suitable selectable markers for bacteria are well known and include resistance genes for ampicillin, kanamycin and tetracycline. Suitable selectable markers for mammalian cells include hygromycin, neomycin, genes that complement a deficiency in the host (*e.g.,* thymidine kinase and TK^{-}cells) and others well known in the art. For yeast cells, one suitable selectable marker is URA3, which confers the ability to grow on medium without uracil.

DNA sequences expressed in this manner may encode a native polypeptide (*e.g.,* human) involved in sphingolipid metabolism or signaling, such as SK, SPL, SPT, or may encode portions or other variants of a native polypeptide involved in sphingolipid metabolism or signaling, such as SK, SPL, SPT or other polypeptides of the present invention described herein. DNA molecules encoding variants of a native polynucleotide may generally be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis, and sections of the DNA sequence may be removed to permit preparation of truncated polypeptides.

To generate cells that express a polynucleotide encoding a polypeptide, such as SPL, SPT, SK, involved in sphingolipid metabolism, cells may be transfected, transformed or transduced using any of a variety of techniques known in the art. Any number of transfection, transformation, and transduction protocols known to those in the art may be used, for example those outlined in *Current Protocols in Molecular Biology*, John Wiley & Sons, New York. N.Y., or in numerous kits available commercially (*e.g.,* Invitrogen Life Technologies, Carlsbad, CA). Such techniques may result in stable transformants

or may be transient. One suitable transfection technique is electroporation, which may be performed on a variety of cell types, including mammalian cells, yeast cells and bacteria, using commercially available equipment. Optimal conditions for electroporation (including voltage, resistance and pulse length) are experimentally determined for the particular host cell type, and general guidelines for optimizing electroporation may be obtained from manufacturers. Other suitable methods for transfection will depend upon the type of cell used (*e.g.,* the lithium acetate method for yeast), and will be apparent to those of ordinary skill in the art. Following transfection, cells may be maintained in conditions that promote expression of the polynucleotide within the cell. Appropriate conditions depend upon the expression system and cell type, and will be apparent to those skilled in the art.

Polypeptides involved in sphingolipid metabolism may be expressed in transfected cells by culturing the cell under conditions promoting expression of the transfected polynucleotide. Appropriate conditions will depend on the specific host cell and expression vector employed, and will be readily apparent to those of ordinary skill in the art. For commercially available expression vectors, the polypeptide may generally be expressed according to the manufacturer's instructions. For certain purposes, expressed polypeptides of this invention may be isolated in substantially pure form. Preferably, the polypeptides are isolated to a purity of at least 80% by weight, more preferably to a purity of at least 95% by weight, and most preferably to a purity of at least 99% by weight. In general, such purification may be achieved using, for example, the standard techniques of ammonium sulfate fractionation, SDS-PAGE electrophoresis, and/or affinity chromatography.

<u>Sphingolipid Intermediates</u>

As noted herein above, the present invention provides agents that modulate the activity of one or more components of a sphingolipid metabolic

and/or signaling pathway. The agents of the present invention also may alter the levels (*e.g.*, relative or absolute amounts, concentrations, stability, or the like) of at least one sphingolipid intermediate. Sphingolipid intermediates of the present invention include any sphingolipid intermediate in the sphingolipid metabolic pathway. As such, the sphingolipid intermediates of the present invention include, but are not limited to, long chain bases (LCBs) and phosphorylated long chain bases (LCBPs) comprising sphingoid backbone structures of between C_{10} and C_{20}. In one embodiment, the backbone structure comprises C_{14}, C_{15}, C_{16}, C_{17}, C_{18}, C_{19}, or C_{20}. In a further embodiment, the sphingolipid intermediates of the present invention include endogenous free sphingoid bases isolated from *Drosophila melanogaster*, including C_{14} and C_{16} sphingosine and C_{14} and C_{16} dihydrosphingosine. In another embodiment, a sphingolipid intermediate comprises any one or more of S-1-P, hexadecanal, phosphoethanolamine, ceramide, sphingosine, 3-keto-dihydrosphingosine, dihydrosphingosine, sphingomyelin, dihydroceramide, ceramide-1-phosphate, dihydrosphingosine-1-phosphate, ethanolamine phosphate, long chain unsaturated aldehyde, and long chain saturated aldehyde. The skilled artisan would readily appreciate that any sphingolipid intermediate species that is affected or generated by any one or more components of the sphingolipid metabolic and/or signaling pathway fall within the scope of the present invention and can be identified using a variety of assays known in the art and further described herein.

Agents that Modulate Sphingolipid Intermediates and/or Components of Sphingolipid Metabolism and/or Signaling

Agents for use according to the present invention are defined as any composition, compound, substance, molecule, material, product or the like, whether artificial or naturally derived, as described herein in further detail, that modulate sphingolipid metabolism and/or signaling. An agent that modulates sphingolipid metabolism and/or signaling is an agent that alters (*e.g.*, increases or

decreases in a statistically significant manner) the level of at least one sphingolipid intermediate or the activity of at least one component of a sphingolipid metabolic and/or signaling pathway. Alteration of a level or activity comprises any statistically significant change, *e.g.* increase or decrease, in the level of one or more intermediates or in the activity of one or more components of sphingolipid metabolism and/or signaling as described herein, when an isolated component, or a host cell or an animal comprising an intermediate or component is contacted with the agent as compared to an isolated component, a host cell or animal comprising an intermediate or component that is not contacted with the agent. As such, in one embodiment, modulation comprises an altered level, *e.g.* a statistically significant decrease or increase in, a polynucleotide encoding a protein involved in sphingolipid metabolism and/or signaling as described herein. Numerous methods for detecting polynucleotide levels (*e.g.* gene expression) are known in the art and are useful in the context of the instant invention. Illustrative methods are described in Ausubel et al. (1993 *Current Protocols in Molecular Biology*, Greene Publ. Assoc. Inc. & John Wiley & Sons, Inc., Boston, MA); Sambrook et al. (1989 *Molecular Cloning*, Second Ed., Cold Spring Harbor Laboratory, Plainview, NY); Maniatis et al. (1982 Molecular Cloning, Cold Spring Harbor Laboratory, Plainview, NY) and elsewhere.

In a further embodiment, modulation comprises an altered activity level, that is a statistically significant decrease or increase in enzymatic activity of any enzyme involved in sphingolipid metabolism and/or signaling, such as SPL, SK, SPT, S-1-PP, and the like. Numerous methods for detecting and measuring enzymatic activity are known in the art and can be used in the context of the present invention (see *e.g.* Current Protocols in Protein Science, John Wiley & Sons, Inc., Boston, MA.). Certain illustrative methods are described in, *e.g.,* Saba, J. D., Nara, F., Bielawska, A., Garrett, S. and Hannun, Y. A. (1997). *J Biol Chem* 272, 26087-26090, and Van Veldhoven, P. P. and Mannaerts, G. P. (1991). *J Biol Chem* 266, 12502-7, Williams, R, Wang E and Merrill A, 1984., *Arch Biochem*

Biophys 228:282-291., Caligan, TB, Peters K, Ou J, Wang E, Saba J and Merrill AH, Jr., 2000. *Analytical Biochemistry* 281:36-44.

In certain embodiments, modulation comprises a statistically significant decrease or increase in the levels of (*i.e.* altered level of) one or more sphingolipid intermediates as described herein, such as S-1-P, ceramide, sphingosine, or other LCBs or LCBPs. A variety of methods for measuring sphingolipid intermediates (*e.g.*, sphingosine-1-phosphate or its degradation products, ceramide, sphingosine, *etc.*) is known in the art and may be useful in the context of the present invention. Illustrative methods are described in the following references: Bose, R and Kolesnick R, 2000. *Methods in Enzymology* 322:373-378; Fyrst, H, *et al.*, 1999, *Biochemistry* 38:5864-5871; Fyrst, H, *et al.*, 1996, *Biochemistry* 35:2644-2650.

In certain embodiments modulation of sphingolipid metabolism and/or signaling comprises an increase or decrease in cellular proliferation, apoptosis, angiogenesis, drug resistance and cell motility. A variety of assays are known in the art to measure these activities, including those described in Current Protocols in Immunology, or Current Protocols in Cell Biology, both published by John Wiley & Sons, Inc., Boston, MA.

Candidate agents of the present invention include polynucleotides encoding polypeptide components of the sphingolipid metabolic and/or signaling pathways such as any of said polypeptide components described herein. Agents of the present invention further include a polypeptide comprising an enzyme involved in sphingolipid metabolism or signaling such as those described herein.

Candidate agents further include any of the sphingolipid intermediates described herein, such as, but not limited to, S-1-P, hexadecanal, phosphoethanolamine, ceramide, sphingosine, 3-keto-dihydrosphingosine, dihydrosphingosine, sphingomyelin, dihydroceramide, ceramide-1-phosphate, dihydrosphingosine-1-phosphate, ethanolamine phosphate, long chain unsaturated aldehyde, and long chain saturated aldehyde. In one embodiment, an

agent of the present invention comprises LCBs and LCBPs such as C_{14} and C_{16} sphingosine and C_{14} and C_{16} dihydrosphingosine identified in the *Drosophila melanogaster* as described herein.

In one particular embodiment, agents of the present invention decrease the level of endogenous S-1-P. Such modulating agents may be identified using methods described herein and used, for example, in cancer therapy and treatment of muscle developmental defects and cardiomyopathy. It has also been found, within the context of the present invention, that the detection of alterations in endogenous S-1-P levels can be used to diagnose cancer and defects in muscle developmental and cardiomyopathy, and to assess the prognosis for recovery. The present invention further provides such diagnostic methods and kits.

Agents which inhibit or block SK activity or expression are also provided in the present invention. In one aspect of the invention, such drugs may be effective treatment for at least some kinds of cancer, especially those in which a dominant Ras mutation is involved. In one embodiment of the invention, such drugs are effective in the treatment of inflammatory and immune disorders. In further embodiments, such drugs may be used as antithrombotic therapy, such as for the therapy of pathologic thrombus formation associated with ischemic heart disease, stroke, vascular disease, angioplasty, and stent deployment. Methods for the identification of new and effective pharmacological agents which inhibit SK activity, as well as drug targets downstream of S-1-P signaling are also provided in the present invention. As used herein, inhibition of SK activity means to decrease the level of SK enzymatic activity as measured using any number of assays known in the art, or certain illustrative assays described herein. Preferably, the decrease in enzymatic SK activity is a statistically significant decrease in enzymatic activity as compared to an appropriate control. Likewise inhibition may apply to the activity of any component of a sphingolipid metabolic and/or signaling pathway, such as SPL, SPT, and the like. In certain embodiments, inhibition of SK activity

is assessed by measuring levels of LCBPs, as described herein in particular in the Examples below.

In certain embodiments, inhibition of SK activity is determined by the ability of an agent to protect or "rescue" a mutant yeast strain from otherwise lethal, toxic and/or growth inhibitory intracellular accumulations of phosphorylated long chain bases (such as S-1-P).

One embodiment of the present invention thus provides agents that inhibit the activity of SK, and related methods and compositions (including mutant and/or recombinant yeast strains) for identifying such agents, for example as determined using one or more yeast screens described herein. In this regard, an agent that rescues certain herein described yeast strains from growth inhibition in the presence of sphingosine (as shown, for example, in Figure 4 and Figure 5) may be a useful agent within the context of the present invention. Thus, an increase in growth of said mutant yeast strain in the presence of sphingosine would be observed in the presence of an illustrative agent. Illustrative agents rescue the mutant yeast strain from growth inhibition in the presence of sphingosine when the growth is altered (*e.g.*, restored, increased) in the presence of sphingosine in a statistically significant manner relative to the growth of the mutant yeast strains in the absence of the agent. Illustrative agents rescue the mutant yeast strain from growth inhibition in the presence of sphingosine when growth is restored in the presence of sphingosine by at least 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5, or 10 fold or higher as compared to mutant yeast strains grown in the absence of the agent. Growth curves can be determined according to methodologies described herein and known to the art, for example, by inoculating synthetic complete media with logarithmically growing cells (of a mutant yeast strain of interest as described herein) to an $O.D._{600\ nm}$ =0.1, then following increase in optical density as a function of time. Controls include mutant cells grown in the absence of sphingosine, mutant cells grown in medium containing sphingosine of various concentrations, mutant cells grown in

medium containing sphingosine of various concentrations plus one of two available known SK inhibitors, N,N-dimethylsphingosine or D,L-*threo*-dihydrosphingosine, and wild type cells in the presence/absence of the inhibitor.

Agents of the present invention that modulate sphingolipid metabolism and/or signaling may be obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides and oligopeptides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available or may be readily produced. Additionally, natural or synthetically produced libraries and compounds can be readily modified through conventional chemical, physical and biochemical means, and may be used to produce combinatorial libraries. Known pharmacological agents may also be subjected to directed or random chemical modifications, such as acylation, alkylation, esterification, amidification, *etc.* to produce structural analogs. New potential therapeutic agents may also be created using methods such as rational drug design or computer modeling.

Illustrative agents of the present invention include arrays of rationally designed chemicals with homology to sphingolipids. In particular, synthetic analogs are created that modulate sphingolipid metabolic and/or signaling pathways. In one embodiment, a rationally designed chemical library includes 1-aryl-2-dimethylaminopropane-1,3-diol derivatives. Derivative is a term understood by the ordinarily skilled artisan. For example, derivative means a compound that can be imagined to arise from a parent compound by replacement of one atom with another atom or group of atoms. Within the context of this invention, these derivatives may be rationally designed. Four diastereomers (D or L, *erythro* or *threo*) are possible for each member of the library. In certain embodiments, the 1-aryl-2 dimethylaminopropane-1,3-diol derivative is derivitized by modifying the amine, the fatty acid amide and the benzene ring of PDMP. In certain

embodiments, the fatty acid amide group is replaced with two N-methyl groups. The skilled artisan would readily appreciate that similar variation can be made in the polar and aromatic substituents to provide other illustrative candidate agents within the context of the instant invention. In another embodiment of the present invention, a 1-aryl-2-dimethylaminopropane-1,3-diol derivative is designed such that lipophilic alkyl groups attached to the arene ring would more closely mimic the character of sphingosine. In one particular embodiment, the synthetic plan makes use of the well-known Garner aldehyde (See **1** in Figure 2) as starting material, since **1** is readily available in either enantiomeric form. In one embodiment, the D- or L-enantiomer of **1** is used as starting material, and pure *erythro* stereoisomers of each library member are prepared. In an additional embodiment, a novel and flexible route for assembling the corresponding *threo* analogues (**4a-c**, Figure 2) is followed using a straightforward extension of methodology for making PDMP analogues. The strategy relies on the *syn*-selective addition to **1** of arylmetal compounds (Aryl-Met) in the presence of certain sulfide and phosphine additives. In this embodiment, both the *erythro* and *threo* synthetic routes are modified to prepare substituted variations at the primary carbon atom. A representative synthetic procedure is shown in Figure 3 for the preparation of **7a-c**. Thus, a wide range of nitrogen, oxygen, and carbon nucleophiles could react with mesylates like **5a-c** and furnish new libraries of dimethylated PDMP analogues and homologues for use as candidates in the context of the present invention.

Candidate agents for use in a method of screening for a modulator of sphingolipid metabolism and/or signaling according to the present invention may be provided as “libraries” or collections of compounds, compositions or molecules. Such molecules typically include compounds known in the art as “small molecules” and having molecular weights less than 10^5 daltons, preferably less than 10^4 daltons and still more preferably less than 10^3 daltons. For example, members of a library of test compounds can be contacted with or administered to a mutant or transgenic yeast strain, or a mutant or transgenic *Drosophila melanogaster* as

described herein, and then assayed for their effects on yeast cell growth and survival, or for their ability to restore the wild type phenotype to mutant and/or transgenic *Drosophila melanogaster*. Compounds so identified as capable of influencing components of the sphingolipid metabolic or signaling pathway (*e.g.,* by altering levels of a sphingolipid intermediate such as S-1-P, ceramide, or sphingosine) may be valuable for therapeutic and/or diagnostic purposes, since they permit treatment and/or detection of diseases associated with sphingolipid metabolism and/or signaling.

Candidate agents further may be provided as members of a combinatorial library, which preferably includes synthetic agents prepared according to a plurality of predetermined chemical reactions performed in a plurality of reaction vessels. For example, various starting compounds may be prepared employing one or more of solid-phase synthesis, recorded random mix methodologies and recorded reaction split techniques that permit a given constituent to traceably undergo a plurality of permutations and/or combinations of reaction conditions. The resulting products comprise a library that can be screened followed by iterative selection and synthesis procedures, such as a synthetic combinatorial library of peptides (see *e.g.,* PCT/US91/08694, PCT/US91/04666) or other compositions that may include small molecules as provided herein (see *e.g.,* PCT/US94/08542, EP 0774464, U.S. 5,798,035, U.S. 5,789,172, U.S. 5,751,629). Those having ordinary skill in the art will appreciate that a diverse assortment of such libraries may be prepared according to established procedures, and tested using the screening methods according to the present disclosure.

Candidate agents of the present invention may also include antibodies that bind to a polypeptide involved in sphingolipid metabolism or signaling. Antibodies may function as modulating agents (as discussed further below) to inhibit or block activity of the polypeptides of the present invention *in vivo*. Alternatively, or in addition, antibodies may be used within screens for

endogenous activity of the polypeptides of the present invention, *e.g.,* SK, SPL, SPT, or modulating agents, for purification of said polypeptides, for assaying the level of activity of said polypeptides within a sample and/or for studies of expression of said polypeptides. Such antibodies may be polyclonal or monoclonal, and are generally specific for one or more polypeptides involved in sphingolipid metabolism and/or one or more variants thereof. Within certain preferred embodiments, antibodies are polyclonal.

Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art (*see, e.g.,* Harlow and Lane, *Antibodies: A Laboratory Manual,* Cold Spring Harbor Laboratory, 1988). In one such technique, an immunogen comprising an SPL polypeptide or antigenic portion thereof is initially injected into a suitable animal (*e.g.,* mice, rats, rabbits, sheep and goats), preferably according to a predetermined schedule incorporating one or more booster immunizations. The use of rabbits is preferred. To increase immunogenicity, an immunogen may be linked to, for example, glutaraldehyde or keyhole limpet hemocyanin (KLH). Following injection, the animals are bled periodically to obtain post-immune serum containing polyclonal antibodies that bind to a polypeptide involved in sphingolipid metabolism, such as SK, SPL, SPT, S-1-PP. Polyclonal antibodies may then be purified from such antisera by, for example, affinity chromatography using a polypeptide of the present invention, such as SK or SPL, or antigenic portion thereof coupled to a suitable solid support. Such polyclonal antibodies may be used directly for screening purposes and for Western blots.

More specifically, an adult rabbit (*e.g.,* NZW) may be immunized with 10 μg purified (*e.g.,* using a nickel-column) SK or SPL polypeptide emulsified in complete Freund's adjuvant (1:1 v/v) in a volume of 1mL. Immunization may be achieved via injection in at least six different subcutaneous sites. For subsequent immunizations, 5 μg of an SK, SPL, or SPT polypeptide may be emulsified in complete Freund's adjuvant and injected in the same manner. Immunizations may

continue until a suitable serum antibody titer is achieved (typically a total of about three immunizations). The rabbit may be bled immediately before immunization to obtain pre-immune serum, and then 7-10 days following each immunization.

For certain embodiments, monoclonal antibodies may be desired. Monoclonal antibodies may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* *6*:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction.

An antibody that specifically binds to a component of a sphingolipid metabolic and/or signaling pathway may interact with said polypeptide component via specific binding if the antibody binds the polypeptide with a K_a of greater than

or equal to about 10^4 M^{-1}, preferably of greater than or equal to about 10^5 M^{-1}, more preferably of greater than or equal to about 10^6 M^{-1} and still more preferably of greater than or equal to about 10^7 M^{-1} to 10^9 M^{-1}. Affinities of binding partners such as antibodies and the polypeptides that they bind to can be readily determined using conventional techniques, for example those described by Scatchard et al., *Ann. N.Y. Acad. Sci. 51*:660 (1949) and in *Current Protocols in Immunology*, or *Current Protocols in Cell Biology*, both published by John Wiley & Sons, Inc., Boston, MA.

As noted above, the present invention provides agents that alter the expression (transcription or translation), stability and/or activity of a polypeptide involved in sphingolipid metabolism. To identify such a modulating agent, any of a variety of screens may be performed. Candidate modulating agents may be obtained using well known techniques from a variety of sources, such as plants, fungi or libraries of chemicals, small molecules or random peptides. Antibodies that bind to a polypeptide of the present invention, and anti-sense polynucleotides that hybridize to a polynucleotides that encodes a protein involved in sphingolipid metabolism, may be candidate modulating agents. Preferably, a modulating agent has a minimum of side effects and is non-toxic. For some applications, agents that can penetrate cells are preferred.

The subject methods find use in the screening of a variety of different potentially therapeutic candidate agents. Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 50 and less than about 2,500 daltons. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional

groups. Candidate agents are also found among biomolecules including, but not limited to: peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof.

Candidate agents of the present invention further include agents that restore wild type phenotype to mutant or transgenic flies as described herein, in particular in the Examples. In one embodiment, modulating agents are screened by culturing or otherwise contacting the agent with a *Drosophila melanogaster* null mutant for a time sufficient to observe in said mutant *Drosophila melanogaster* an effect of the agent on a level of either at least one sphingolipid intermediate, or the activity of at least one component of sphingosine metabolism and/or signaling pathway. The term "null allele" is a term of art meaning an allele that makes no gene product or whose product has no activity of any kind. Thus a null mutant is a mutant comprising a null allele. In one embodiment, the *Drosophila melanogaster* null mutant has a flightless phenotype caused by abnormal development of indirect flight muscles (IFM) during metamorphosis. This phenotype provides a novel schema by which to elucidate sphingolipid metabolism and signaling, identify genetic suppressors and identify chemicals which modulate sphingolipid metabolism and/or signaling through their effect on key components in the sphingolipid metabolic and/or signaling pathway. Agents that result in a statistically significant alteration in the level of a sphingolipid intermediate or alteration in the level of activity of a component of a sphingolipid metabolic or signaling pathway is an agent that modulates sphingolipid metabolism and/or signaling. Agents that result in a statistically significant restoration in the phenotype of a mutant or transgenic fly grown or otherwise cultured in the presence of said agent as compared to a mutant or transgenic fly grown or otherwise cultured in the absence of the agent as described herein is an agent that modulates sphingolipid metabolism and/or signaling.

As mentioned above, the subject mutant and transgenic flies find particular utility in screening assays designed to identify diagnostic and therapeutic

compounds for a variety of human diseases as described herein, such as numerous cancers including breast, colon, uterus, stomach, ovary, lung, kidney and rectal cancer, and diagnosis and treatment of hereditary sensory neuropathy type 1 and the sphingolipidoses. Through use of the subject transgenic flies (or cells derived therefrom depending on the particular screening assay), one can identify compounds that have activity with respect to sphingolipid metabolism and/or signaling and therefore, the diseases associated with modulation of sphingolipid metabolism and/or signaling. Compounds have activity with respect to sphingolipid metabolism and/or signaling if they modulate or have an effect on at least one parameter or symptom of the disease, such as tumor development, *etc.*, where the modulatory activity may be to reduce or enhance the magnitude of the symptom. Tumors comprise abnormal masses of tissue and can be benign or cancerous. As would be readily appreciated by the skilled artisan, there are dozens of different types of tumors and their identification and diagnosis are known in the art and can be determined by a qualified clinician.

Thus, the screening methods of subject invention can be used to identify compounds that modulate the progression of disease, *e.g.* by binding to, modulating, enhancing or repressing the activity of a protein or peptide involved in the sphingolipid metabolism and/or signaling, and/or compounds that ameliorate, alleviate or even remove the phenotypic symptoms of the disease, where such activity may or may not be the result of activity with respect to the underlying mechanism of the disease.

Assays of the invention make it possible to identify compounds which ultimately: (1) have a positive affect with respect to diseases associated with sphingolipid metabolism and/or signaling and as such are therapeutics, *e.g.*, agents which arrest or reverse development of tumors or ameliorate or alleviate the symptoms of such a condition; or (2) have an adverse affect with respect to the disease and as such should be avoided as therapeutic agents.

In certain preferred screening methods of the subject invention, a quantity of a candidate agent is generally orally administered to the fly. Following oral administration, the affect of the candidate agent on phenotype of the fly is determined, typically by comparison with a control (*i.e.* a mutant or transgenic fly to which the candidate agent has not been administered). The effect of the candidate agent is determined by determining whether one or more of the phenotypic characteristics of the mutant or transgenic fly as described herein are exacerbated or ameliorated in the test fly as compared to the control fly, where characteristics that are monitored include levels of sphingolipid intermediates, flight behavior, flight muscle developmental defects, and the like. The candidate agent is generally orally administered to the fly by mixing the agent into the fly nutrient medium and placing the medium in the presence of the fly, (either the larva or adult fly) such that the fly feeds on the medium. Generally a plurality of assay mixtures are run in parallel with different candidate agent concentrations (or no candidate agent) to obtain a differential response to the various concentrations of the candidate agent. Typically, one of these test groups serves as a negative control, *i.e.*, no candidate agent is present. In a preferred embodiment, a high throughput screening protocol is employed, in which a large number of candidate agents are tested in parallel using a large number of flies. By "large number" is meant a plurality, where plurality means at least 50, usually at least 100, and more usually at least 1000, where the number of may be 10,000 or 50,000 or more, but in many instances will not exceed 5000.

A modulating agent may additionally comprise, or may be associated with, a targeting component that serves to direct the agent to a desired tissue or cell type. As used herein, a "targeting component" may be any substance (such as a compound or cell) that, when linked to a compound enhances the transport of the compound to a target tissue, thereby increasing the local concentration of the compound. Targeting components include antibodies or fragments thereof, (*e.g.* anti-tumor antibodies) receptors, ligands and other molecules that bind to cells of,

or in the vicinity of, the target tissue. Known targeting components include hormones, antibodies against cell surface antigens, lectins, adhesion molecules, tumor cell surface binding ligands, steroids, cholesterol, lymphokines, fibrinolytic enzymes and other drugs and proteins that bind to a desired target site. In particular, anti-tumor antibodies and compounds that bind to an estrogen receptor may serve as targeting components. An antibody employed in the present invention may be an intact (whole) molecule, a fragment thereof, or a functional equivalent thereof (*e.g.* antigen-binding fragments). Examples of antibody fragments are F(ab')2, -Fab', Fab and F[v] fragments, which may be produced by conventional methods or by genetic or protein engineering. Linkage may be via any suitable covalent bond using standard techniques that are well known in the art. Such linkage is generally covalent and may be achieved by, for example, direct condensation or other reactions, or by way of bi- or multi-functional linkers.

Assays for Detecting Modulation of Components of Sphingolipid Metabolism and/or Signaling and/or Sphingolipid Intermediates

Numerous assays for detecting modulation of components of sphingolipid metabolism and/or signaling are available in the art. Illustrative assays are described further herein, for example as described in the Example section.

Numerous methods for detecting polynucleotides of the present invention are known in the art and are useful in the context of the instant invention. Illustrative methods are described in Ausubel et al. (1993 *Current Protocols in Molecular Biology*, Greene Publ. Assoc. Inc. & John Wiley & Sons, Inc., Boston, MA); Sambrook et al. (1989 *Molecular Cloning*, Second Ed., Cold Spring Harbor Laboratory, Plainview, NY); Maniatis et al. (1982 Molecular Cloning, Cold Spring Harbor Laboratory, Plainview, NY), and elsewhere. In one embodiment, polynucleotide expression is measured using any number of hybridization techniques. In further embodiments, polynucleotide expression is measure using

amplification techniques, such as RT-PCR, PCR, quatitative-competitive (QC) PCR, and real-time PCR.

Numerous methods for detecting and measuring enzymatic activity of components involved in sphingolipid metabolism and/or signaling are known in the art and can be used in the context of the present invention (see *e.g.* Current Protocols in Protein Science, John Wiley & Sons, Inc., Boston, MA.). Certain illustrative methods are described in Saba, J. D., Nara, F., Bielawska, A., Garrett, S. and Hannun, Y. A. (1997). *J Biol Chem* 272, 26087-26090, and Van Veldhoven, P. P. and Mannaerts, G. P. (1991). *J Biol Chem* 266, 12502-7, Williams, R, Wang E and Merrill A, 1984., *Arch Biochem Biophys* 228:282-291., Caligan, TB, Peters K, Ou J, Wang E, Saba J and Merrill AH, Jr., 2000. *Analytical Biochemistry* 281:36-44.

In one embodiment, SK activity of an SK polypeptide or variant thereof may generally be assessed using an *in vitro* assay that detects the production of labeled substrate (*i.e.,* sphingosine-1-phosphate, or a derivative thereof). SK is responsible for the phosphorylation of sphingosine to generate S-1-P. In one embodiment of the present invention, an *in vitro* assay for SK requires both ATP and a divalent cation (magnesium, calcium or manganese) for the phosphorylation of the hydroxyl group on the first carbon of sphingosine. SK activity may be assayed in tissues from a variety of species, including human and porcine platelets, bovine brain and kidney, rat liver, the yeast *Hansenula ciferrii*, and *Tetrahymena pyriformis*. In one embodiment, the assay requires a fixed ratio of magnesium to ATP of 5:1 and a neutral pH (between 7.2-7.5). SK is found in the cytoplasm of platelets and is associated with membranes in rat brain and several other tissues. D-*erythro*-sphingosine, the naturally occurring isomer of sphingosine and most abundant sphingoid base in most mammalian cells, serves as a substrate for SK from all sources. Sphingosine inhibits the activity of protein kinase C, and stereospecificity for the *erythro* conformation has been demonstrated in mixed micellar assays using human platelet and rat brain-derived

enzyme. A variety of long chain bases can also serve as substrates for SK, including *erythro*-dihydrosphingosine and phytosphingosine. SK activity increases with the carbon chain length of a D-*erythro*-dihydrosphingosine substrate. In one embodiment, stimulation of Swiss 3T3 cells with some inducers of proliferation (fetal calf serum or PDGF) can be used to assay an increase in both sphingosine levels and SK activity. Illustrative stimuli which can be used to activate SK include nerve growth factor, muscarinic acetylcholine agonists, TNFα, and cross-linking of the FcεRI and FcγRI immunoglobulin receptors. Additional mitogens such as the b subunit of the cholera toxin and 12-O-tetradecanoyl phorbol-13-acetate may also be used to increase SK enzyme activity.

Within certain embodiments, an *in vitro* assay for SK activity may be performed using cellular extracts prepared from cells that express a polypeptide of interest. Preferably, in the absence of a polynucleotide encoding an SK polypeptide, such cells do not produce a significant amount of endogenous SK (*i.e.,* a cellular extract should not contain a detectable increase in the level of SK, as compared to buffer alone without extract). Illustrative assays for detection of SK activity are known in the art, such as those described herein in the Examples.

Screens for modulating agents that alter expression or stability of a polypeptide of the present invention may be readily performed using well known techniques that detect the level of protein or mRNA. Suitable assays include RNAse protection assays, *in situ* hybridization, ELISAs, Northern blots and Western blots. Such assays may generally be performed using standard methods (*see* Sambrook et al., *Molecular Cloning: A Laboratory Manual,* Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). For example, to detect mRNA encoding SK, SPL or other polynucleotides involved in the metabolism of sphingolipids, a nucleic acid probe complementary to all or a portion of the gene sequence of interest may be employed in a Northern blot analysis of mRNA prepared from suitable cells. Additionally, *In situ* hybridization may be performed as described in Blair, S. (Blair S., 2000. Imaginal discs. *In Drosophila* Protocols.

W. Sullivan, M. Ashburner, and R. Hawley, editors. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY. 159-175).

Alternatively, real-time PCR can also be used to detect levels of mRNA encoding SPL, SK, or other polypeptides involved in sphingolipid metabolism as described herein (*see* Gibson et al., *Genome Research* 6:995-1001, 1996; Heid et al., *Genome Research* 6:986-994, 1996). The first-strand cDNA to be used in the quantitative real-time PCR is synthesized from 20μg of total RNA that is first treated with DNase I (*e.g.*, Amplification Grade, Gibco BRL Life Technology, Gaitherburg, MD), using Superscript Reverse Transcriptase (RT) (*e.g.*, Gibco BRL Life Technology, Gaitherburg, MD). Real-time PCR is performed, for example, with a GeneAmp™ 5700 sequence detection system (PE Biosystems, Foster City, CA). The 5700 system uses SYBR™ green, a fluorescent dye that only intercalates into double stranded DNA, and a set of gene-specific forward and reverse primers. The increase in fluorescence is monitored during the whole amplification process. The optimal concentration of primers is determined using a checkerboard. The PCR reaction is performed in 25μl volumes that include 2.5μl of SYBR green buffer, 2μl of cDNA template and 2.5μl each of the forward and reverse primers for the SPL gene, or other gene of interest. The cDNAs used for RT reactions are diluted approximately 1:10 for each gene of interest and 1:100 for the β-actin control. In order to quantitate the amount of specific cDNA (and hence initial mRNA) in the sample, a standard curve is generated for each run using the plasmid DNA containing the gene of interest. Standard curves are generated using the Ct values determined in the real-time PCR which are related to the initial cDNA concentration used in the assay. Standard dilution ranging from $20\text{-}2\times10^6$ copies of the SPL gene or other gene of interest are used for this purpose. In addition, a standard curve is generated for β-actin ranging from 200fg-2000fg. This enables standardization of the initial RNA content of a sample to the amount of β-actin for comparison purposes. The mean copy number for each sample tested is normalized to a

constant amount of β-actin, allowing the evaluation of the observed expression levels of SPL or other genes of interest.

To detect a protein of the present invention, a reagent that binds to the protein (typically an antibody, as described herein) may be employed within an ELISA or Western assay. Following binding, a reporter group suitable for direct or indirect detection of the reagent is employed (*i.e.*, the reporter group may be covalently bound to the reagent or may be bound to a second molecule, such as Protein A, Protein G, immunoglobulin or lectin, which is itself capable of binding to the reagent). Suitable reporter groups include, but are not limited to, enzymes (*e.g.*, horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. Such reporter groups may be used to directly or indirectly detect binding of the reagent to a sample component using standard methods known to those of ordinary skill in the art.

Alternatively, or in addition, a candidate modulating agent may be tested for the ability to alter enzymatic activity, such as SPL or SK activity, using an *in vitro* assay as described herein (*see* Van Veldhoven and Mannaerts, *J. Biol. Chem.* *266*:12502-07, 1991) that detects the degradation of labeled substrate (*i.e.*, sphingosine-1-phosphate, or a derivative thereof). Briefly, a solution (*e.g.*, a cellular extract) containing an SK or SPL polypeptide (*e.g.*, 10 nM to about 10 mM) may be incubated with a candidate modulating agent (typically 1 nM to 10 mM, preferably 10 nM to 1 mM) and a substrate (*e.g.*, 40 μM) at 37°C for 1 hour in the presence of, for example, 50 mM sucrose, 100 mM K-phosphate buffer pH 7.4, 25 mM NaF, 0.1% (w/v) Triton X-100, 0.5 mM EDTA, 2 mM DTT, 0.25 mM pyridoxal phosphate. Reactions may then be terminated and analyzed by thin-layer chromatography to detect the formation of labeled fatty aldehydes and further metabolites. A modulating agent (*e.g.*, an antibody or other modulating agent as described herein) that alters SK or SPL activity results in a statistically significant increase or decrease in the degradation of sphingosine-1-phosphate, relative to

the level of degradation in the absence of modulating agent. Such modulating agents may be used to increase or decrease SK or SPL activity in a cell culture or a mammal, as described herein.

Modulating agents that alter the SPL activity of an SPL polypeptide or variant thereof may generally be assessed using an *in vitro* assay that detects the degradation of labeled substrate (*i.e.*, sphingosine-1-phosphate, or a derivative thereof). Within such assays, pyridoxal 5'-phosphate is normally a requirement for SPL activity. In addition, the reaction generally proceeds optimally at pH levels around 7.4-7.6 and requires chelators due to sensitivity toward heavy metal ions. PH levels may be from 6.5, 6.7, 6.9, 7.0, 7.1, 7.2, 7.3, 7.7, 7.8, 7.9, 8.0, 8.1, 8.2, 8.3, 8.4, or 8.5. The substrate should be a D-*erythro* isomer, but in derivatives of sphingosine-1-phosphate the type and chain length of sphingoid base may vary. In general, an assay as described by Van Veldhoven and Mannaerts, *J. Biol. Chem.* *266*:12502-07, 1991 may be employed. Briefly, a solution (*e.g.*, a cellular extract) containing the polypeptide may be incubated with about 40 μM substrate at 37°C for about 1 hour in the presence of, for example, 50 mM sucrose, 100 mM K-phosphate buffer pH 7.4, 25 mM NaF, 0.1% (w/v) Triton X-100, 0.5 mM EDTA, 2 mM DTT, 0.25 mM pyridoxal phosphate. Reactions may then be terminated and analyzed by thin-layer chromatography to detect the formation of labeled fatty aldehydes and further metabolites. A modulating agent as described herein that alters SPL activity of an SPL polypeptide or variant thereof will result in a statistically significant increase or decrease in SPL activity as assayed herein as compared to the activity in the absence of said modulating agent.

Within certain embodiments, an *in vitro* assay for SPL activity may be performed using cellular extracts prepared from cells that express the polypeptide of interest. Preferably, in the absence of a gene encoding an SPL polypeptide, such cells do not produce a significant amount of endogenous SPL (*i.e.*, a cellular extract should not contain a detectable increase in the level of SPL, as compared to buffer alone without extract). It has been found, within the context

of the present invention, that yeast cells containing deletion of the SPL gene (*BST1*) are suitable for use in evaluating the SPL activity of a polypeptide. *bst1*Δ cells can be generated from *S. cerevisiae* using standard techniques, such as PCR, as described herein. A polypeptide to be tested for SPL activity may then be expressed in *bst1*Δ cells, and the level of SPL activity in an extract containing the polypeptide may be compared to that of an extract prepared from cells that do not express the polypeptide. For such a test, a polypeptide is preferably expressed on a high-copy yeast vector (such as pYES2, which is available from Invitrogen) yielding more than 20 copies of the gene per cell. In general, a polypeptide has SPL activity if, when expressed using such a vector in a *bst1*Δ cell, a cellular extract results in a two-fold increase in substrate degradation over the level observed for an extract prepared from cells not expressing the polypeptide.

A further test for SPL activity may be based upon functional complementation in the *bst1*Δ strain. It has been found, within the context of the present invention, that *bst1*Δ cells are highly sensitive to D-*erythro*-sphingosine. In particular, concentrations as low as 10 μM sphingosine completely inhibit the growth of *bst1*Δ cells. Such a level of sphingosine has no effect on the growth of wildtype cells. A polypeptide having SPL activity as provided above significantly diminishes (*i.e.,* by at least two fold) the sphingosine sensitivity when expressed on a high-copy yeast vector yielding more than 20 copies of the gene per cell.

The present invention also provides yeast assays for the identification of agents that modulate sphingolipid metabolism and/or signaling. In one embodiment, the present invention provides yeast assays for the identification of agents that modulate SK activity. In one embodiment, the growth of yeast mutant strains lacking any one or more of SPL, SK and SPP activity, and/or activity of one or more other components of the sphingolipid metabolic and/or signaling pathway as described herein, is inhibited by the presence of sphingosine. In certain embodiments, the yeast mutant strain comprises a null allele in DPL1 and LCB4. (As noted above, the term "null allele" is a term of art

meaning an allele that makes no gene product or whose product has no activity of any kind. Thus a null mutant is a mutant comprising a null allele). In another embodiment, the yeast mutant strain comprises a null allele in DPL1, LCB4, and YSR2. In a further embodiment, the yeast mutant strain comprises a null allele in YSR2 and SUR2. In yet a further embodiment, the yeast mutant strain comprises a null allele in at least one or more of DPL1, LCB4, YSR2, and SUR2. In yet another embodiment, the mutant yeast strain for use in screening agents that modulate sphingolipid metabolism and/or signaling is further transformed or transfected to express nonendogenous SK (*e.g.*, from an exogenous source, a source other than from yeast, such as human, mouse, *Drosophila melanogaster*, *C. elegans)* such as SK derived from human, mouse, or from other sources, such as *Drosophila melanogaster*, *C. elegans*, *etc*. In certain related embodiments, a mutant yeast strain is genetically modified to express nonendogenous SPL, SPP, SPT, or one or more other components of the sphingolipid metabolic and/or signaling pathway. In one embodiment, the nonendogenous component of the sphingolipid metabolic and/or signaling pathway, such as SK, SPL, SPP, or SPT, is expressed under the control of an inducible promoter, such as a galactose inducible promoter. In this context, the assay includes the appropriate concentration of galactose in the growth media. In one embodiment, inhibition of SK activity by a candidate agent leads to the rescue of the phenotype from sensitivity to sphingosine or to an inducer (*e.g.*, galactose) that induces expression of a nonendogenous component of the sphingolipid metabolic and/or signaling pathway, and allows for growth of the yeast strain in the presence of sphingosine or the inducer.

In one particular embodiment, the screen for agents that modulate sphingolipid metabolism and/or signaling, such as inhibitors of SK, is performed on agar plates containing between about 10 to about 200 μM D-*erythro*-sphingosine. In one embodiment, the agar plates contain between about 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 50, 51,

52, 53, 54, 55, 56, 57, 58, 59, 60, 65, or 70 μM D-*erythro*-sphingosine, or appropriate concentration of any other long chain sphingoid base that inhibits growth of the mutant yeast strains described herein. Agar plates may further contain an appropriate concentration of dispersant, such as NP40 at about 0.0015%. In one embodiment the screen for agents that modulate sphingolipid metabolism and/or signaling, such as agents that inhibit SK activity, is performed in a 96-well plate. In this context, small, equal numbers of mutant yeast cells are placed into each well, and an array of candidate agents as described herein are diluted into the wells prior to incubation. As would be recognized by the skilled artisan, cell numbers and the concentration of candidate agents can be optimized experimentally. Generally, concentration of sphingosine and cells are kept constant. In certain embodiments, growth curves are determined by inoculating the appropriate growth medium, such as synthetic complete medium with logarithmically growing cells to an $O.D._{600nm}$ of about 0.1, then following increase in optical density as a function of time. As noted above, in certain embodiments, the appropriate growth medium may include galactose or the appropriate inducer for an inducible promoter. The lowest inhibitory concentration of sphingosine is determined. Controls for optimization include mutant yeast strain in sphingosine of various concentrations plus known SK inhibitors, such as N,N-dimethylsphingosine or D,L-*threo*-dihydrosphingosine, and wild type cells in the presence and absence of these inhibitors.

Generally, illustrative agents rescue the growth inhibition of a mutant yeast strain in the presence of any long chain sphingoid base that inhibits growth of a mutant yeast strain, such as D-*erythro*-sphingosine, when the mutant strain growth is restored in the presence of a growth inhibitory long chain sphingoid base in a statistically significant manner as compared to mutant yeast strains grown in the absence of the agent. In one embodiment, the long chain sphingoid base that inhibits growth of a mutant yeast strain as described herein is D-*erythro*-sphingosine. In certain embodiments, the growth of a mutant yeast strain in the

presence of sphingosine in the appropriate growth medium is restored in the presence of a candidate agent, by at least 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5, or 10 fold or higher as compared to mutant yeast strains grown in the absence of the agent.

In certain embodiments illustrative agents rescue the growth inhibition of a mutant yeast strain in the presence of an inducer that induces expression of a nonendogenous gene (*e.g.*, a nonendogenous component of the sphingolipid metabolic and/or signaling pathway, such as SK, SPL, SPP, or SPT) from an inducible promoter. Thus, in certain embodiments, expression of the nonendogenous gene results in growth inhibition of a mutant yeast strain (*e.g.* even in the absence of sphingosine in the growth media). Illustrative inducible promoters include but are not limited to galactose-inducible promoters and thus, an illustrative inducer in this context is galactose. Illustrative candidate agents include agents that restore mutant strain growth in the presence of the appropriate inducer (*e.g.*, galactose) in a statistically significant manner as compared to mutant yeast strains grown in the absence of the candidate agent.

The skilled artisan would readily appreciate that any variety of inducible promoters and their cognate inducers can be used in the context of the present invention. A variety of inducible systems can be used, including galactose-inducible promoters, pXyl-*xylR*-inducible promoter, the pSpac-*lacI* system, the arabinose-inducible P_{BAD} promoter and a tetracycline-inducible promoter system using, for example, the *xyl/tetO* promoter. Other illustrative inducible promoters that can be used in the context of the present invention are activated by physical means such as the heat shock promoter. Others are activated by (*i.e.*, the inducers are) chemicals such as IPTG or Tetracycline. Thus, in certain embodiment of the invention the nucleic acid molecule encoding a desired protein such as SK, SPL, SPP, or SPT is under the control of an inducible control element (*e.g.*, a promoter) such that expression of the desired protein can be turned on or off (or intermediate levels in between) using an inducer which affects the

inducible control element (*e.g.*, expression can be modulated by modulating the concentration of the inducer in the presence of the yeast strain). This allows for switching on or off of the expression of the protein. A variety of inducible promoters and their cognate inducers are commercially available, for example, from Invitrogen Life Technologies (Carlsbad, CA) or Stratagene (La Jolla, CA). Other illustrative inducible or otherwise regulated expression systems include but are not limited to those controlled by heavy metals (Mayo et al. 1982 Cell 29:99-108), RU-486 (a progesterone antagonist) (Wang et al. 1994 Prxoc. Natl. Acad. Sci. USA 91:8180-8184), steroids (Mader and White, 1993 Proc. Natl. Acad. Sci. USA 90:5603-5607), and tetracycline (Gossen and Bujard 1992 Proc. Natl. Acad. Sci. USA 89:5547-5551; U.S. Pat. No. 5,464,758).

In certain embodiments, the plate assay utilizes two available SK inhibitors, N,N-dimethylsphingosine and D,L-*threo*-dihydrosphingosine (Yatomi, Y., et al., *Biochemistry* 1996, 35(2), 626-633; Stoffel, W. & Bister, K. *Hoppe-Seyler's Z Physiol Chem* 1973, 354, 169-181.) Concentrations of D-*erythro*-sphingosine that inhibit cell growth overnight (at 30^0C with shaking) can be determined by measuring turbidity at OD_{600nm}, or by any other appropriate means, such as counting cells on a hemacytometer. D-*erythro*-sphingosine concentrations that inhibit growth of a specific number of inoculated cells except in the presence of SK inhibitors are chosen as conditions for screening.

In certain embodiments, the assay to screen for modulators of sphingolipid metabolism and/or signaling can be further validated in a *dpl1 lcb4 lcb5* strain containing murine SphK1 cDNA (GenBank Accession No. AF068748) (Kim, S., Fyrst, H. & Saba, J. *Genetics* 2000, 156, 1519-1529). Chemicals promoting growth of this strain in sphingosine can be validated using survival assays on agar plates containing the chemical. The efficacy and biochemical characteristics of candidate compounds may be quantified by using any number of assays, such as 1) determining the IC_{50} of the inhibitor on purified SK and recombinant human SK, 2) analyzing the kinetics of inhibition using classical

Michaelis-Menten methods, 3) determining the reversibility of the inhibition and/or 4) by comparing the LCBP accumulation of a *dpl1 human SK* strain treated with no inhibitor versus treatment with a known SK inhibitors versus treatment with the new compound. *In vitro* SK assays are performed using an HPLC based assay as described in Caligan, et al., (*supra*).

In certain embodiments, in order to validate a yeast mutant strain screen for modulators of sphingolipid metabolism and/or signaling, the mutant yeast strains as described herein are inoculated to a density of about 1 x 10^4 cells per plate onto agar plates containing about 100 μM D-*erythro*-sphingosine and about 0.0015% NP40 (used as a dispersant). At these concentrations of sphingosine and this cell density, the *dpl1Δ* yeast strains do not grow. Similarly, plates containing D-*erythro*-sphingosine *plus* known SK inhibitors may be incubated for 3-5 days, and plates inspected for sphingosine resistance. If it appears that the strain containing human SK can survive sphingosine in the presence of SK inhibitors, a dilutional assay provides semi-quantitative information on the degree of protection afforded by the known inhibitors. For the sphingosine dilutional assay, cells are grown to saturation for about 2-3 days in liquid cultures and then resuspended in minimal medium, placed in the first row of a 96 well plate and diluted serially from about 1:2 to about 1:4000 across the plate. The cultures are then template-inoculated onto a control plate (rich medium) and a plate containing 50 μM sphingosine and 0.0015% NP40, plus or minus SK inhibitor (At this concentration of NP40, no effects on cell viability are observed.) Plates are then incubated at 30°C for about 2 days and assessed visually for differences in growth.

Assays to detect and measure sphingolipid intermediates include solid phase extraction. In certain embodiments, a Strata C18-E solid phase extraction column (50 mg/ml) (Phenomenex, Torrance, CA) can be used. In this context the column is initially wetted with 200 μl of methanol, followed by equilibration with 1 ml of solvent A. Fly extracts or LCB standards in solvent A may

be applied to the equilibrated Strata C18-E column, followed by a wash with 1 ml of solvent A. A second wash of the column is performed by the addition of 600 µl of methanol. LCBs are then eluted from the column with 600 µl of methanol:10 mM ammonium acetate, 9:1 (v/v) and dried down in a speed vac. The skilled artisan would readily appreciate that the above parameters can be optimized and changed according to extracts and LCBs being used.

High-performance liquid chromatography analysis (HPLC) can also be used within the context of the present invention. HPLC can be carried out as described for example in Lester, R. L., and R. C. Dickson. 2001. *Anal. Biochem.* **298:** 283-292. Briefly, LCBs are derivatized with, for example, *ortho*-phthalaldehyde (OPA) (Sigma St. Louis, MO) as described in Caligan, T. B., K. Peters J. Ou, E. Wang, J. Saba, and A. H. Jr. Merrill. 2000. *Anal. Biochem.* **281:** 36-44. The OPA-derivatized LCBs are separated on a reverse-phase column with the mobile phase methanol/10 mM ammonium acetate, pH 5.2, 82:18 (v/v). Numerous reverse-phase columns are known in the art. Illustrative reverse-phase columns include but are not limited Luna RP-18, 3 µ, 4.6 x 75 mm (Phenomenex, Torrance, CA). Flow rate is generally in the range of 1 ml/min. The skilled artisan would appreciate that flow rates can range from 0.2 ml/min to 3 ml/min and include any integer in between. Any number of HPLC systems can be used. Illustrative systems include a Beckman System Gold with a 125 solvent module. Fluorescent LCBs can be detected using a variety of systems. In one particular embodiment, fluorescent LCBs are detected and quantified using a Spectra-Physics fluorescence detector (SP 8410).

Mass Spectrometry may also used in the context of the present invention to detect and measure sphingolipid intermediates as described herein. In one particular embodiment, a Strata C18-E column-purified lipid extract from a desired source, and a C_{14} sphingolipid standard are analyzed on a Micromass Quattro LCZ instrument following direct injection of 10 µl of sample. Mobile phase is generally in the range of 80 percent methanol containing 0.1 percent formic

acid. The skilled artisan would appreciate that the mobile phase can be optimized. Flow rate is generally in the range of 0.2 ml/min. Structural confirmation of LCBs is obtained by positive electrospray ionization (ESI+) mass spectrometry. LCBs can be detected by precursor ion scans of structurally distinct ion fragments as described in the art, in particular as described in Sullards, M. C., and A. H. Jr. Merrill. 2001. *Sci. STKE.* **67:** 1-11. Generally, 3.5 kV is applied to the capillary to start the spray and the collision-induced decomposition spectra, at a cone voltage of 20 V, are recorded at a collision energy of 15 eV with argon as collision gas. The skilled artisan would readily understand that any of the above parameters can change according to different samples and desired intermediates being measured as is known in the art.

Thus, LCBs can be identified through their patterns of collision-induced dissociation and precursor ion scans using positive ion electrospray mass spectrometry (ESI+) as described in Sullards, M. C., and A. H. Jr. Merrill. 2001. *Sci. STKE.* **67:** 1-11. Based on their unique molecular structures, typical decomposition products arise from the loss of two water molecules. For example, the precursor ion spectrum of m/z 208 (C_{14} sphingosine minus two water molecules) shows parents as m/z 244 (C_{14} sphingosine) and m/z 226 (C_{14} sphingosine minus one water molecule). In order to verify the existence of, for example C_{14} dihydrosphingosine in *Drosophila melanogaster*, a Strata C18-E column purified lipid extract may be analyzed by ESI+. In addition, precursor ion scans of m/z 236 and m/z 238 identify C_{16} sphingosine and C_{16} dihydrosphingosine in a sample.

Lipid extracts for analysis in the context of the present invention can be prepared using any number of procedures known in the art. For example, to prepare *Drosophila melanogaster* lipid extracts, samples containing 25 mg of frozen intact fly material are placed in a homogenizer, for example a 7 ml Potter Elvehjem homogenizer. 20 µl of a mixture of internal LCB standards, (commercially available from, for example Matreya Inc., Pleasant Gap, PA)

containing 250 to 500 pmol of each LCB are then added. Flies are homogenized in 2 ml of ice cold methanol/water, 1:1 (v/v) with a loose pestle followed by a tight pestle until it moved smoothly. Extracts are further homogenized with a tip sonicator (3 x 20 sec.) while on ice, then transferred to a glass tube and centrifuged at 1500 x g for 10 minutes. Supernatants are recovered and dried down in a speed vac. Extracts are resuspended in 200 µl of methanol containing 0.1 M ammonium hydroxide, followed by vortexing, bath sonication and incubation at 37• C for 1 hr to allow hydrolysis of esterified acyl chains. Following hydrolysis, the samples are cooled to room temperature, dried down in a speed vac and resuspended in 500 µl of methanol/water, 2:3 (v/v) containing 0.1% glacial acetic acid (solvent A). The skilled artisan would recognize that the above procedure may be modified accordingly to prepare lipid extracts from other samples including mammalian cells, yeast, bacteria or any other desired source of sphingolipid intermediate.

As noted herein, sphingolipid signaling contributes to specific pathways for biological signal transduction, including those associated with cell division, cell survival, apoptosis, proliferation and differentiation and "biological signal transduction pathways" or "inducible signaling pathways" in the context of the present invention include transient or stable associations or interactions among molecular components involved in the control of these and similar processes in cells. Depending on the particular sphingolipid signaling pathway of interest, such as a pathway induced by S-1-P binding to an EDG receptor and the like, an appropriate parameter for determining induction of such pathway may be selected. Signaling pathways associated with cell proliferation, there is available a variety of well known methodologies for quantifying proliferation, including, for example, incorporation of tritiated thymidine into cellular DNA, monitoring of detectable (*e.g.,* fluorimetric or colorimetric) indicators of cellular respiratory activity, or cell counting, or the like. Similarly, in the cell biology arts there are known multiple techniques for assessing cell survival (*e.g.*, vital dyes, metabolic

indicators, *etc.*) and for determining apoptosis (*e.g.,* annexin V binding, DNA fragmentation assays, caspase activation, *etc.*). Other signaling pathways will be associated with particular cellular phenotypes, for example specific induction of gene expression (*e.g.,* detectable as transcription or translation products, or by bioassays of such products, or as nuclear localization of cytoplasmic factors), altered (*e.g.,* statistically significant increases or decreases) levels of intracellular mediators (*e.g.,* activated kinases or phosphatases, altered levels of cyclic nucleotides or of physiologically active ionic species, *etc.*), or altered cellular morphology, and the like, such that cellular responsiveness to a particular stimulus as provided herein can be readily identified to determine whether a particular cell responds to a particular sphingolipid signaling pathway.

Methods for Detecting Cancer

Within other aspects, the present invention provides methods and kits for diagnosing cancer and/or identifying individuals with a risk for developing cancer or with a risk for metastasis that is higher or lower than average. It has been found, within the context of the present invention, that certain human tumor cells contain an altered SK and SPL expression. In particular, decrease SPL expression was observed in certain tumor tissues as compared to corresponding normal tissue from the same individual, as described further in the Examples. Further, increase SK expression was observed in numerous tumor tissues as compared to corresponding normal tissue from the same individual. In other words, such polynucleotides or the proteins encoded by these polynucleotides, may be used as markers to indicate the presence or absence of a cancer in a patient.

Thus, one aspect of the present invention provides methods for detecting cancer by detecting alterations in expression level of polynucleotides encoding components of a sphingolipid metabolic and/or signaling pathway, in particular SK and SPL. In this regard, an individual demonstrating a statistically

significant decrease in expression of SPL as compared to a control is considered to be afflicted with a cancer. In particular, a 50% to 60%, 61%, 62%, 63%, 64%, or 65% reduction in SPL expression in a cancer sample as compared to a corresponding normal tissue indicates the presence of cancer in a patient. In one embodiment, a 20%, 30%, 35%, 40%, 45%, 46%, 47%, 48%, or 49% reduction in SPL expression in a cancer sample as compared to a corresponding normal tissue indicates the presence of cancer in a patient. Likewise, an individual demonstrating a statistically significant increase in expression of SK as compared to a control is considered to be afflicted with a cancer. In particular, a 50% to 60%, 61%, 62%, 63%, 64%, or 65% increase in SK expression in a cancer sample as compared to a corresponding normal tissue indicates the presence of cancer in a patient. In one embodiment, a 20%, 30%, 35%, 40%, 45%, 46%, 47%, 48%, or 49% increase in SK expression in a cancer sample as compared to a corresponding normal tissue indicates the presence of cancer in a patient.

A cancer may be detected based on the level of mRNA encoding a protein involved in sphingolipid metabolism an/or signaling in a biological sample obtained from an individual suspected of having a cancer as compared to the level of mRNA detected in a biological sample obtained from a normal control subject known to be free of cancer. In certain embodiments, biological samples which contain cDNA pairs representing tumor tissue and corresponding normal tissue from the same patient can be used to determine the presence of cancer, for example as described in the examples. By utilizing sample (*e.g.*, cell, tissue or biological fluid) pairs from one patient, differences between gene expression in tumor and normal tissue which might be due to person-to-person variability should not confound the interpretation of results. In certain other embodiments, samples may be obtained both from a subject suspected of having or being at risk for having cancer (*e.g.*, a patient) and from a normal, control subject known to be free of the presence and/or risk for having cancer (*e.g.*, a malignancy). Those familiar with the art will appreciate that for the described or characterized cancers, clinical

criteria have been established for ascertaining when one or more signs or symptoms are apparent at levels upon which a suspicion that cancer is present may be based. A biological sample may include, but is not limited to, blood, sera, urine, cells or tissue of any type such as breast, lung, colon and the like, biopsy, tumor, lymph node, and the like. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay (*e.g.* RT-PCR, QC-RT-PCR, real-time PCR, *etc.*) to amplify a portion of a cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.,* hybridizes to specifically as determined using any one of a variety of techniques and controls known in the art) a polynucleotide encoding the protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Generally, the oligonucleotide primers used in this context can be generated using guidelines known in the art. In particular, oligonucleotide primers are designed such that they are specific for a polynucleotide of interest. The PCR conditions used can be optimized in terms of temperature, annealing times, extension times and number of cycles depending on the oligonucleotide and the polynucleotide to be amplified. Such techniques are well know in the art and are described in for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, *51*:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989). Oligonucleotide primers can be anywhere from 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides in length. In certain embodiments, the oligonucleotide primers of the present invention are 35, 40, 45, 50, 55, or 60 nucleotides in length. In one embodiment, the oligonucleotides comprise a sequence described herein, such as those set forth in SEQ ID NOs:1, 3, 5, 7, 9, 12, 15, 17, and 22-27, or the complement thereof.

Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a protein involved in sphingolipid metabolism an/or signaling may be used in a hybridization assay to detect the presence of

polynucleotide encoding said protein in a biological sample as described herein (biological sample may include, but is not limited to, blood, tissue, biopsy, tumor, lymph node, and the like) obtained from a patient suspected of having cancer. Oligonucleotide probes can be of the lengths as described above. In certain embodiments, a probe may comprise the entire sequence as set forth in SEQ ID NOs: 1, 3, 5, 7, 9, 12, 15, 17, and 22-27, or the complement thereof.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a protein of the invention that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes hybridize to a polynucleotide encoding a polypeptide described herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence as disclosed herein. Techniques for both PCR based assays and hybridization assays are well known in the art (*see*, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, *51*:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning

two orders of magnitude. A statistically significant increase or decrease in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive. Alternatively, levels of polynucleotide in corresponding normal tissues from the same test patient may be used as controls.

One aspect of the present invention provides methods for monitoring the progression of a cancer by detecting alterations in expression level of polynucleotides encoding components of a sphingolipid metabolic and/or signaling pathway, in particular SK and SPL. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected shows a statistically significant increase (such as for SK) or decrease (such as for SPL) over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant with time.

Specific alterations present in the genes encoding the polypeptides of the present invention involved in sphingolipid metabolism in other tumor cells, such as breast, colon, uterine, or other tumor cells, may be readily identified using standard techniques, such as PCR. Alterations that may be associated with a particular tumor include amino acid deletions, insertions, substitutions and combinations thereof. Methods in which the presence or absence of such an alteration is determined may generally be used to detect cancer and to evaluate the prognosis for a patient known to be afflicted with cancer.

To detect an altered gene, any of a variety of well-known techniques may be used including, but not limited to, PCR and hybridization techniques, using polynucleotides of the present invention, or variants thereof. Any sample that may

contain cancerous cells may be assayed. In general, suitable samples are tumor biopsies. Within a preferred embodiment, a sample is a breast tumor biopsy.

Kits for diagnosing or evaluating the prognosis of a cancer generally comprise reagents for use in the particular assay to be employed. In general, a kit of the present invention comprises one or more containers enclosing elements, such as primers, probes, reagents or buffers, to be used in an assay. For example, a kit may contain one or more polynucleotide primers or probes comprising at least 15 nucleotides complementary to a polynucleotide encoding a polypeptide involved in sphingolipid metabolism. In a preferred embodiment, said polypeptide is SK. In certain embodiments, the primers or probes comprise at least 10, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95 or 100 nucleotides, and preferably at least 150 or 200 nucleotides, complementary to an mRNA or to a polynucleotide encoding a polypeptide involved in sphingolipid metabolism. Such probe(s) may be used to detect, for example, an altered SK gene by hybridization. For example, a kit may contain one probe that hybridizes to a region of an SK or SPL gene that is not generally altered in tumors (a control) and a second probe that hybridizes to a region commonly deleted in breast cancer. A sample that contains mRNA that hybridizes to the first probe, and not to the second (using standard techniques) contains an altered SK or SPL gene. Suitable control probes include probes that hybridize to a portion of the SK or SPL gene outside of a deleted region. Alternatively, a kit may comprise one or more primers for PCR analyses, which may be readily designed based upon the sequences provided herein by those of ordinary skill in the art. Optionally, a kit may further comprise one or more solutions, compounds or detection reagents for use within an assay as described above.

In a related aspect of the present invention, kits for detecting a polypeptide involved in sphingolipid metabolism are provided. Such kits may be designed for detecting the level of protein or nucleic acid encoding a protein, *e.g.* SK or SPL, within a sample, or may detect the level of SK or SPL activity as

described herein. A kit for detecting the level of SK or SPL, or nucleic acid encoding SK or SPL, or other component of sphingolipid metabolism and/or signaling as described herein, typically contains a reagent that binds to the protein, DNA or RNA. To detect nucleic acid encoding SK, SPL or other protein, the reagent may be a nucleic acid probe or a PCR primer. To detect SK, SPL, or other protein, the reagent is typically an antibody. The kit may also contain a reporter group suitable for direct or indirect detection of the reagent as described above.

Generation of Mutant and Transgenic *Drosophila melanogaster*

The invention further provides mutant and/or transgenic *Drosophila melanogaster*. In one embodiment, a mutant *Drosophila melanogaster* comprises a P-element transposon insertion in a coding region of a gene encoding a component of a sphingolipid metabolic and/or signaling pathway. In certain embodiments, the P-element transposon insertion results in an altered level (*e.g.*, a statistically significant increase or decrease) of at least one sphingolipid intermediate as described herein. In a further embodiment, the P-element transposon results in altered activity level of at least one sphingolipid pathway component as described herein. In further embodiments, the mutant *Drosophila melanogaster* of the present invention comprise a P-element insertion in the coding region of more than one gene encoding a component of a sphingolipid metabolic and/or signaling pathway. Mutants can be generated comprising any number of insertions in any number of genes encoding components of a sphingolipid metabolic and/or signaling pathway. In certain embodiments, 1, 2, 3, 4, or 5 genes encoding components of a sphingolipid metabolic and/or signaling pathway contain P-element insertions.

Illustrative lines of *Drosophila melanogaster* include Wild type Canton S, $lace^{2}/lace^{05305}$ and Sply mutant lines. Flies can be obtained from the Drosophila Genome Project Stock Center (Bloomington, IN). General fly

husbandry is known in the art and is described for example, in Ashburner, M and Roote J, 2000. Laboratory culture of *Drosophila*, *Drosophila Protocols* 585-600. Analysis of *Drosophila melanogaster* anatomical structures may be carried out by the skilled artisan using a variety of techniques in the art, including those described in (O'Donnell, P. T. and Bernstein, S. I. (1988). *J Cell Biol* **107**, 2601-12.; Fyrberg, E. A., Bernstein, S. I. and VijayRaghavan, K. (1994). *Methods Cell Biol* **44**, 237-58.).

The invention further provides *Drosophila melanogaster* mutants that exhibit a flightless phenotype, where the phenotype results from the disruption of an endogenous gene involved in sphingolipid metabolism and/or signaling, for example, the SPL, SK, SPT, or other gene as described in detail herein. In one embodiment, flightless phenotype is meant that the subject non-mammalian organism models spontaneously develop a reduced number of muscle fibers comprising the dorsal longitudinal muscles (DLM) and have compensatory hypertrophy in the remaining fibers. Analysis of DLM formation is carried using markers specific for different stages of differentiation, as well as GFP markers which distinguish myoblasts emerging from imaginal discs versus larval template muscles. Expression of a series of markers of muscle development can also be used in evaluating embryonic muscle differentiation. For example, Dmef2 is expressed in migrating myoblasts, allowing analysis of early steps in embryonic myogenesis. These myoblasts divide, forming two myocytes that express αMHC and ultimately fuse to form embryonic muscles. Thus, by evaluating αMHC, embryonic muscle fusion can be evaluated.

In certain aspects, the *Drosophila melanogaster* mutant of the present invention may also demonstrate abnormal developmental patterning of thoracic muscles of the T2 segment. Identification of *Drosophila melanogaster* anatomy is readily carried out by the skilled artisan using a variety of techniques knows in the art, including those described in the Examples herein, or, for example, Developmental Biology, 6th Edition, Scott F. Gilbert, Sinauer Associates,

Inc., Sunderland, MA. In a preferred embodiment, the above phenotypes result in an inability to fly or otherwise reduced flight performance as described in the Examples or as described in Vigoreaux, et al., 1993 J. Cell Biol. May; 121(3):587-98. The subject *Drosophila melanogaster*, within a preferred embodiment, demonstrate altered activity of at least one component of a sphingolipid metabolic and/or signaling pathway, such as SPL, SK, SPT, ceramidase or other component as described herein. In a particularly illustrative embodiment, said *Drosophila melanogaster* has decreased activity of endogenous SPL and/or increased or decreased activity of SK.

In a preferred embodiment, the strain contains a mutation in any one or more of the genes encoding a component of the sphingolipid metabolism and/or signaling, such as SPL, SK, SPT, S-1-PP, ceramidase, or any combination thereof. In a further embodiment of the present invention the *D. melanogaster* strain are heterozygous for a P-element transposon which sits in any region of the gene encoding the SPL protein set forth in SEQ ID NO:16. In a certain embodiment, the P-element transposon sits in a regulatory region of the gene. In a preferred embodiment, the flies are homozygous insertional mutants in the coding region of the gene encoding the SPL protein set forth in SEQ ID NO:16. In a further embodiment of the present invention the *D. melanogaster* strain are heterozygous for a P-element transposon which sits in the coding region of the gene encoding the SK protein set forth in any one of or all of SEQ ID NOs:18, 19, 20, 28, and 29. In a preferred embodiment, the flies are homozygous insertional mutants in the coding region of the gene encoding the SK protein set forth in any one or more of SEQ ID NOs:18, 19, 20, 28, and 29. In yet a further embodiment of the present invention, the homozygous mutant strain of fly has a flightless phenotype. In certain embodiments, the mutant flies have a reduced number of muscle fibers comprising the dorsal longitudinal muscles and have compensatory hypertrophy in the remaining fibers. In certain aspects, the mutant flies of the present invention may also demonstrate abnormal developmental patterning of

thoracic muscles of the T2 segment, for example as described herein in the Examples. Identification of normal and abnormal anatomy of the *Drosophila melanogaster* can be carried out using techniques known to the skilled artisan and described herein, and for example, in Developmental Biology, 6th Edition, Scott F. Gilbert, Sinauer Associates, Inc., Sunderland, MA. Illustrative mutant flies have altered sphingolipid metabolism.

Flies heterozygous for a P-element transposon which sits in a gene encoding a component of sphingolipid metabolism and/or signaling may be obtained from the *Drosophila* Genome Project. Homozygous insertional mutants can be made, using techniques known in the art, by genetically crossing and evaluating progeny for the presence of homozygous insertional mutants (for example, based on presence of rosy eye color, encoded by a recessive marker carried on the P-element). Expression of the SPL or other gene involved in sphingolipid metabolism, can be evaluated using any number of assays known to the skilled artisan, for example, by Northern blot analysis. To determine the SPL function of each genotype, +/+, +/- and -/- flies may be homogenized using standard techniques and whole extracts can be assayed for SPL activity using assays as described herein. The transposon can be mobilized by crossing SPL mutant flies with flies carrying an actively transcribed transposase gene, which should cause the P-element to be excised in the chromosomes of both somatic cells and in the germline. Germline transposon loss is heritable and can be identified in progeny by virtue of eye color or other relevant marker. Progeny which lost both the transposase gene and the P-element can then be isolated and the restored allele can be homozygosed.

Mutations in *Drosophila melanogaster* as described herein which permanently block expression of a functional protein can be created in several ways, such as with P-element transposon insertions or chemical or radiation induced mutagenesis. Exemplary strains of mutant flies are available through the *Drosophila* Genome Project, at the University of California at Berkeley (Adams, M.

et al 2000. The genome sequence of *Drosophila melanogaster*. *Science*. 287:2185-2195.). Alternatively, insertional mutant of interest may be obtained by using local hop strategies essentially as described in Tower, J. et al (Tower, J., et al. 1993. Preferential transposition of *Drosophila* P elements to nearby chromosomal sites. *Genetics*. 133:347-359.). Transposons can be mobilized by crossing in a transposase gene, followed by crossing the transposase back out (reintroducing genetic stability). Mutant flies can be identified using techniques know to those of skill in the art. For example, mutant flies can be identified by probing Southern blots prepared from extracts from flies generated in the screen using the target gene as probe. Subsequently, crosses can be performed to introduce a mutant allele of interest, (*e.g.* SPL, SK, SPT or other component of sphingolipid metabolism and/or signaling) and generate homozygosity at both mutant alleles (*e.g.* SPL *and* new transposon integration sites). Mutants can be screened for a phenotype of interest, for example the ability to restore flight to an SPL mutant when the mutated allele is homozygous (predicting a recessive phenotype).

In one aspect of the present invention, fly genetic manipulation may entail mating or "crossing" of flies and selection for or against progeny expressing various phenotypic markers. Exemplary techniques for fly genetic manipulation of the present invention are know in the art and are described, for example in, Ashburner, M., and J. Roote. 2000. Laboratory culture of *Drosophila*. *In Drosophila* Protocols. W. Sullivan, M. Ashburner, and R. Hawley, editors. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY. 585-600. Phenotypic markers may be used to identify the inheritance of chromosomes, engineered transposable elements, or transposase genes used to facilitate their mobilization. Marker mutations affecting eye color, bristle shape, wing morphology and cuticle pigmentation, for example, may be employed in the crosses for the mutant flies of the present invention. Within one aspect of the present invention, it may be desirable to select the individuals which contain a collection of markers indicating

the desired genotype. In another aspect of the present invention, balancer chromosomes may be used to create the ability to identify recessive mutations present in the heterozygous state. Balancer chromosomes may be employed to prevent homologous recombination during meiotic prophase in females. The presence of both dominant and recessive lethal markers allows one to determine the presence or absence of the balancer chromosomes and simultaneously to follow the homologous chromosomes, which may themselves not contain a dominant marker. One particularly illustrative cross of the present invention is to eliminate the P-element insertion in the *Drosophila melanogaster* SPL gene and establish phenotypic reversion, as described herein in the Examples.

The genetics required to create the mutant flies described herein may involve several successive steps. For example, lines homozygous for the *Sply*^{05091} allele and the *lace*^{05305} allele can to be generated by meiotic recombination. *Sply*^{05091} and *lace*^{05305} mutations can be introduced in trans and balanced in the next generation. Flies carrying the *lace*^{05305} allele can be selected by the presence of w^+. Presence of *Sply*^{05091} and other mutation of the present invention can be verified by PCR. Similar strategies are employed to create other strategic crosses envisioned by the present invention. For example, lines containing null alleles for both SK genes will be generated. Lines containing null alleles for one or more components of a sphingolipid metabolic and/or signaling pathway are envisioned by the present invention. For example, lines containing null alleles for SK and SPL are envisioned. Lines containing null alleles for SPT and SK are envisioned as are other double, triple, and quadruple mutant lines of virtually any component in a sphingolipid metabolic and/or signaling pathway.

Selective markers to allow for selection of mutant flies is provided for in the present invention. Exemplary selective markers of the present invention may comprise a wild type rosy (ry^+) allele carried on the transposon to allow for selection for or against the stable transposon. Introduction of an active transposase is selected for by presence of, for example, the dominant marker,

Stubble (short bristle phenotype) in the first cross, and is selected against to identify progeny which have lost the transposase, restoring genetic stability in the second cross. Other illustrative markers include Curly O (CyO) which is lethal when present in two copies, allowing selection for heterozygotes containing the CyO balancer and another allele of interest originally containing the transposon (*e.g.*, SPL). By selecting against rosy eye color, progeny in which the transposon has been excised from the locus of interest, *e.g.*, SPL, SK, or other components of sphingolipid metabolism and/or signaling can be identified. Expansion of this "reverted" allele in the population can be achieved in the third cross, and the desired allele can be homozygosed in the final cross, to determine whether restoration of the intact allele of interest, for example SPL and/or SK, is associated with a desired phenotype of interest, such as restoration of flight.

Transgenic *Drosophila melanogaster* are also provided in the present invention. Relevant methods of preparing transgenic *Drosophila melanogaster* are disclosed in: Spradling, A. C., and Rubin, G. M. (1982). Science 218, 341-347; Brand & Perrimon, Development (1993) 118: 401-415; and Phelps & Brand, Methods (April 1998) 14:367-379. See also, Spradling A C, P Element Mediated Transformation in *Drosophila*: A Practical Approach (ed. D. D. Roberts, IRL Press, Oxford)(1986) pp 175-179; and U.S. Patent No. 6, 316,690.

The subject transgenic flies can be prepared using any convenient protocol that provides for stable integration of the transgene in to the fly genome in a manner sufficient to provide for the requisite spatial expression of the transgene. A number of different strategies can be employed to obtain the integration of the transgene with the requisite expression pattern. Generally, methods of producing the subject transgenic flies involve stable integration of the transgene into the fly genome. Stable integration is achieved by first introducing the transgene into a cell or cells of the fly, *e.g.* a fly embryo. The transgene is generally present on a suitable vector, such as a plasmid. Transgene introduction may be accomplished using any convenient protocol, where suitable protocols include: electroporation,

microinjection, vesicle delivery, *e.g.* liposome delivery vehicles, and the like. Following introduction of the transgene into the cell(s), the transgene is stably integrated into the genome of the cell. Stable integration may be either site specific or random, but is generally random.

Where integration is random, the transgene is typically integrated with the use of transposase. In such embodiments, the transgene is introduced into the cell(s) within a vector that includes the requisite P element, terminal 31 base pair inverted repeats. Where the cell into which the transgene is to be integrated does not comprise an endogenous transposase, a vector encoding a transposase is also introduced into the cell, *e.g.* a helper plasmid comprising a transposase gene, such as pTURBO (as disclosed in Steller & Pirrotta, "P Transposons Controlled by the Heat Shock Promoter," Mol. Cell. Biol. (1986) 6:1640-1649). Methods of random integration of transgenes into the genome of a target *Drosophila melanogaster* cell(s) are disclosed in U.S. Pat. No. 4,670,388.

In those embodiments in which the transgene is stably integrated in a random fashion into the fly genome, means are also provided for selectively expressing the transgene at the appropriate time during development of the fly. In other words, means are provided for obtaining targeted expression of the transgene. To obtain the desired targeted expression of the randomly integrated transgene, integration of particular promoter upstream of the transgene, as a single unit in the P element vector may be employed. Alternatively, a transactivator that mediates expression of the transgene may be employed. Of particular interest is the GAL4 system described in Brand & Perrimon, *supra*.

In one aspect of the present invention, transgenic flies can be created using P-elements to express, overexpress or misexpress proteins of interest, such as SPL, SK, SPT, S-1-PP, ceramidase, or any combination thereof. The transgenes for use in the context of the present invention may include SPL, SK, SPT, S-1-PP, ceramidase, or any other protein involved in sphingolipid metabolism and/or signaling from human, mouse, yeast, or *C. elegans*. In further

embodiments of the present invention, the transgene of interest comprises a polynucleotide encoding a fusion protein. For example, a polynucleotide encoding a polypeptide component of the sphingolipid metabolic pathway, such as SK, SPL, SPT, S-1-PP and the like, can be engineered to fuse the protein of interest to a marker protein such as GFP for use as a transgene in the context of this invention. The skilled artisan would readily recognize that any number of marker proteins can be used in fusion proteins of the present invention.

In one embodiment of the invention, GAL4-mediated ectopic gene expression is employed, essentially as described (van Roessel, P., and A. Brand. 2000. GAL4-mediated ectopic gene expression in *Drosophila*. *In Drosophila* Protocols. W. Sullivan, M. Ashburner, and R. Hawley, editors. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY. 439-448.). Other illustrative inducible promoter may be used as well, such as those described in Rubin, G, Hong L, Brokstein P, Evans-Holm M, Frise E, Stapleton M and Harvey D, 2000. A *Drosophila* complementary DNA resource, *Science* 287:2222-2224. The GAL4 protein is a yeast transcription factor capable of activating transcription of *Drosophila melanogaster* genes which have been engineered to contain upstream sequences recognized by the GAL4 protein. Various mutants can be created with a gene of interest expressed in specific tissue distributions, a construct containing the gene of interest (reporter) under regulation of a GAL4 containing promoter is introduced into embryos, and a genetic marker allows identification of progeny containing this construct. Illustrative GAL4 containing promoters include, but are not limited to, pUAS. The skilled artisan would readily appreciate that other inducible systems can be used in the context of the present invention. The use of embryos of a strain containing an active P-transposase increases the efficiency of transgene integration, although many of the embryos die. These progeny can then be crossed to various available lines containing GAL4 transgenes (driver) expressed under control of tissue-specific promoters. In one embodiment of the

present invention, GAL4 driver constructs which allow expression during embryogenesis may be used.

Various methods to identify the etiology of the SPL, SPT and other mutant phenotypes are known to those of skill in the art and are also provided herein. The present invention provides for mutant *Drosophila melanogaster* with defective or overexpressed SPL, SK, SPT and S-1-P phosphatase genes. In a particular embodiment, abnormal sphingolipid metabolism is a phenotype of the mutant *Drosophila melanogaster* of the present invention. In a further embodiment, the abnormal sphingolipid metabolism affects developmental programs in the mutant flies. In certain embodiments, the mutant and/or transgenic *Drosophila melanogaster* of the present invention develop one or more tumors. Tumors can be identified and measured using a variety of techniques known to the skilled artisan. Particularly illustrative techniques are described in, for example, De Lorenzo, C., B.M. Mechler, and P.J. Bryant. 1999. *Cancer Metastasis Rev.* 18:295-311.; Watson, K., R. Justice, and P. Bryant. 1994. *J Cell Sci Supp.* 18:19-33. ; Gateff, E., and H. Schneiderman. 1967.. *Amer Zool.* 7:760.; Gateff, E. 1994. *Int J Dev Biol.* 4:565-590, or any references cited therein.

Quantitative analysis and characterization of sphingolipids in normal and mutant and/or transgenic flies throughout development may be carried out using any number of techniques known to the skilled artisan. Such techniques are described in, for example, Ashburner, M., and J. Roote. 2000, Laboratory culture of *Drosophila. In Drosophila* Protocols, W. Sullivan, M. Ashburner, and R. Hawley, editors, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY. Pp. 585-600; Blair, S. 2000, Imaginal discs, *In Drosophila* Protocols, W. Sullivan, M. Ashburner, and R. Hawley, editors. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY. 159-175, and Stern, D., and E. Sucena. 2000. Preparation of larval and adult cuticles for light microscopy. *In Drosophila* Protocols. W. Sullivan, M. Ashburner, and R. Hawley, editors. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY. 601-616.

Further, identification of lipids which are not within normal concentration ranges in various mutants of the present invention, especially those demonstrating developmental defects, can be done using standard techniques. In certain embodiments, the embryonic, larval, pupal and adult stages of development of *Drosophila melanogaster* models harboring single or multiple sphingolipid metabolic defects are examined using techniques described herein, in particular in the Examples. Light and electron microscopy and *in situ* hybridization with appropriate tissue-specific markers of differentiation should identify both gross and subtle defects associated with altered sphingolipid metabolism.

Within further aspects, the present invention provides other transgenic organisms in which sphingolipid metabolism is altered, compared to wild-type organisms. Within the context of the present invention, organisms may include but are not limited to mice, rats, and *C. elegans*, and other species of *Drosophila*. Such organisms may contain an alteration, insertion or deletion in an endogenous gene involved in sphingolipid metabolism and/or signaling, or may contain DNA encoding a modulating agent that modulates expression or activity of a gene involved in sphingolipid metabolism. In one embodiment the altered endogenous gene comprises SK. In certain aspects, such organisms may contain DNA encoding a modulating agent that increases expression or activity of an SK or an SPL gene. Transgenic organisms may be generated using techniques that are known to those of ordinary skill in the art. For example, a transgenic organism containing an insertion or deletion in the coding region for the SK or SPL gene may be generated from embryonic stem cells, using standard techniques. Such stem cells may be generated by first identifying the full genomic sequence of the gene encoding the SK or SPL, and then creating an insertion or deletion in the coding region in embryonic stem cells. Alternatively, appropriate genetically altered embryonic stem cells may be identified from a bank. Using the altered stem cells, hybrid organisms may be generated with one normal SK or SPL gene and one

marked, abnormal gene. These hybrids may be mated, and homozygous progeny identified.

Transgenic organisms may be used for a variety of purposes, which will be apparent to those of ordinary skill in the art. For example, such organisms may be used to prepare cell lines from different tissues, using well known techniques. Such cell lines may be used, for example, to evaluate the effect of the alteration, and to test various candidate modulators.

In addition to their use as animal models for screening candidate therapeutic agents, the subject mutant and transgenic flies also find use in the identification of gene targets involved in sphingolipid metabolism and/or signaling, *i.e.* genes whose expression can be beneficially modulated to treat diseases associated with sphingolipid metabolism and/or signaling. Gene based therapies can be identified by doing traditional enhancer/suppressor analyses in the subject mutant and transgenic flies. In these analyses, genes in the subject mutant and/or transgenic flies are mutated to identify ones that either exacerbate or alleviate the mutant or transgenic phenotype. Methods of mutating genes and carrying out enhancer/suppressor analyses are well known to those of skill in the art (Hays, T S et al., Molecular and Cellular Biology (March 1989) 9(3):875-84; Deuring, R; Robertson, B; Prout, M; and Fuller, M T. Mol. Cell. Biol., 1989 9:875-84.; Fuller, M T et al., Cell Mot. Cyto. (1989) 14 :128-35; Rottgen G, Wagner T, Hinz U Mol. Gen. Genet. 1998 257:442-51).

Genes that mutate to enhance the phenotype of mutant and/or transgenic flies of the present invention in a recessive manner yield potential protein therapeutics for conditions associated with sphingolipid metabolism and/or signaling, since elevating the normal gene product level of such genes potentially alleviates such condition. Genes that mutate to suppress the adult onset neurodegeneration phenotype in a recessive manner yield gene targets for disruption to alleviate the diseases associated with sphingolipid metabolism or signaling, where disruption of these genes can be achieved using a variety of

methods, ranging from deleting the DNA for the target gene to inhibiting its transcription, translation, or protein activity. For screening candidate agents, small molecule antagonists to these genes can be constructed and evaluated for efficacy in the fly model through oral administration. Alternatively, large molecular antagonists can be delivered by gene therapy, as described infra.

Generation of Mutant Yeast Strains

As noted above, according to certain embodiments, the present invention provides mutant strains of yeast, in particular *Saccharomyces cerevisiae*, having one or more mutated and/or transformed components of a sphingolipid metabolic and/or signaling pathway, and methods of using such yeast strains to identify agents that modulate sphingolipid metabolism and/or signaling. Other yeast which can be used in practicing the present invention are *Neurospora crassa*, *Aspergillus niger*, *Aspergillus nidulans*, *Pichia pastoris*, *Candida tropicalis*, and *Hansenula polymorpha*. The term "yeast", as used herein, includes not only yeast in a strictly taxonomic sense, *i.e.*, unicellular organisms, but also yeast-like multicellular fungi or filamentous fungi. In particular, according to certain preferred embodiments, the present invention provides mutant strains of yeast comprising at least one mutation in at least one gene encoding any component of the sphingolipid metabolic and/or signaling pathway. In this regard a mutation may comprise an insertion, a deletion, a knockout allele, a null allele, a dominant negative mutation, or any other mutation that modifies the native sequence of the gene so as to modulate the activity of the component of sphingolipid metabolic and/or signaling pathway. In one embodiment, a mutant strain of yeast comprises a disruption mutant in one or more genes encoding a component of sphingolipid metabolism and/or signaling. In this context, the mutant yeast strains of the present invention include strains containing null alleles of one or more of the genes encoding any component of the sphingolipid metabolic and/or signaling pathway including, but not limited to, SPL (DPL1), SK (LCB4 and/or LCB5), SPP

(YSR2 and/or YSR3), a gene that catalyzes the conversion of dihydrosphingosine to phytosphingosine (SUR2), ceramidase, SPT, and the like. In one embodiment, the mutant yeast strain comprises *dpl1Δ*. In a further embodiment, the mutant yeast strain comprises a *dpl1, ysr2* double mutant. In a further embodiment, the mutant yeast strain comprises a *dpl1, ysr2, lcb4* triple mutant. In one embodiment, the mutant yeast strains have a phenotype characterized by sensitivity to long chain sphingoid bases, such as D-*erythro*-sphingosine. In certain embodiments, the mutant yeast strain is characterized by intracellular accumulation of LCBPs.

In certain embodiments, the mutant yeast strains are transformed with one or more polynucleotides encoding one or more components of the sphingolipid metabolic and/or signaling pathway. In one particular embodiment, the mutant yeast strains are transformed with one or more polynucleotides encoding one or more nonendogenous (*e.g.*, of non yeast origin or derived from a source different from the mutant yeast strain) components of the sphingolipid metabolic and/or signaling pathway. In this regard, the polynucleotides may be derived from human, mouse, *C. elegans*, *D. melanogaster*, or other species. In certain embodiments, a mutant yeast strain is transformed with a polynucleotide encoding human SK (SPHK1), mouse SK, *C. elegans* SK, or *D. melanogaster* SK. In another embodiment, a mutant yeast strain of the present invention is transformed with a polynucleotide encoding human SPL, ceramidase, SPP, SPT, 3-keto dihydrosphingosine reductase, ceramide synthase, sphingosine desaturase, ceramide kinase, phosphoethanolamine cytidylyltransferase, CDP-ethanolamine phosphotransferase, acid sphingomyelinase, sphingomyelin synthase, neutral sphingomyelinase, oxosphinanine reductase, and/or glucosylceramide synthase. In yet a further embodiment, a mutant yeast strain of the present invention is transformed with a polynucleotide encoding a human intracellular or cell surface receptor, such as any one or more of the EDG receptors (*e.g.* EDG1, EDG3, EDG5, EDG6, EDG8) or CFTR. As noted above,

the murine, *C. elegans*, and *D. melanogaster* homologs of the above polynucleotides may also be included within the context of this invention.

Polynucleotides for use in transforming mutant yeast strains as described herein may be cloned using standard techniques into any expression vector suitable for use within the yeast strain and transformed into the host cell using techniques well known to those of ordinary skill in the art, such as the lithium acetate method (Ito, H., Fukuda, Y., Murata, K. and Kimura, A. (1983). *J Bacteriol* 153, 163-8.). As is readily appreciated by the skilled artisan, the polynucleotide encoding the polypeptide of interest is cloned into the expression vector such that it is operably linked to the promoter such that the polypeptide of interest is properly translated and expressed as a functional protein. In certain embodiments, the promoter used is an inducible promoter, *e.g.* a galactose inducible promoter. A number of vectors exist for the expression of recombinant proteins in yeast. For instance, YEP24, YIP5, YEP51, YEP52, pYES2, and YRP17 are cloning and expression vehicles useful in the introduction of genetic constructs into *S. cerevisiae* (see, for example, Broach et al. (1983) in Experimental Manipulation of Gene Expression, ed. M. Inouye Academic Press, p. 83). These vectors can replicate in *E. coli* due the presence of the pBR322 ori, and in *S. cerevisiae* due to the replication determinant of the yeast 2 micron plasmid. In addition, drug resistance markers such as ampicillin may be used. Moreover, if yeast are used as a host cell, it will be understood that the expression of a gene in a yeast cell may require a promoter which is functional in yeast. Suitable promoters include the promoters for metallothionein, 3-phosphoglycerate kinase (Hitzeman et al., *J. Biol. Chem.* 255, 2073 (1980) or other glycolytic enzymes (Hess et al., *J. Adv. Enzyme Req.* 7, 149 (1968); and Holland et al. *Biochemistry* 17, 4900 (1978)), such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phospho-fructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phospho-glucose isomerase, and glucokinase. Suitable vectors and promoters for use in

yeast expression are further described in R. Hitzeman et al., EPO Publication No. 73,657. Other promoters, which have the additional advantage of transcription controlled by growth conditions, are the promoter regions, alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, and the aforementioned metallothionein and glyceraldehyde-3-phosphate dehydrogenase, as well as enzymes responsible for maltose and galactose utilization. Illustrative expression vectors for use in the present invention include pYES (Invitrogen, Carlsbad, CA). Finally, promoters that are active in only one of the two haploid mating types may be appropriate in certain circumstances. Among these haploid-specific promoters, the pheromone promoters MFa1 and MF.alpha.1 are of particular interest.

In certain embodiments, the ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are generally located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Optionally, the construct may contain an enhancer, a transcription terminator, a poly(A) signal sequence, a bacterial or mammalian origin of replication and/or a selectable marker, all of which are well known in the art. Enhancer sequences may be included as part of the promoter region or separately. Transcription terminators are sequences that stop RNA polymerase-mediated transcription. The poly(A) signal may be contained within the termination sequence or incorporated separately. A selectable marker includes any gene that confers a phenotype on the host cell that allows transformed cells to be identified. Such markers may confer a growth advantage under specified conditions. Suitable selectable markers for yeast cells include but are not limited to URA3 which confers the ability to grow on medium without uracil, and LEU2.

Illustrative methods for generating and growing mutant yeast strains are described, for example, in Sherman, F., *et al.* 1986, *Methods in Yeast Genetics*. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY; Kim and Saba, 2000 *Genetics* 156:1519-1529; Saba, J., *et al.*, 1997. *J. Biol. Chem.* 272:26087-26090; Skrzypek, M., et al., 1999 *J. Bacteriol.* 181:1134-1140; and Lanterman and Saba, 1998 *Biochem. J.* 332:525-531. In particular, disruption or deletion procedures to mutate genes of interest with PCR-amplified disruption constructs are described for example in Baudin, A. *et al.*, 1993 *Nucleic Acids Res.* 21:3329-3330; Lorenz, M.C., *et al.*, 1995 *Gene* 158:113-117; and Wach, A., *et al.*, 1994 *Yeast* 10:1793-1808. In certain embodiments, transposon mutagenesis is employed in which cells are transformed with a plasmid containing a transposable element, and the genomic location of the gene into which the transposon had inserted is determined using any number of assays including genetic suppressor screens as described herein.

Methods of Use and Pharmaceutical Compositions

The agents that modulates a component of sphingolipid metabolism and/or signaling and/or a sphingolipid intermediate as described herein are useful for the detection, diagnosis and treatment of any disease associated with altered sphingolipid metabolism and/or signaling. Illustrative diseases include but are not limited to a variety of cancers (*e.g.* breast, colon, uterus, stomach, ovary, lung, kidney and rectum cancer), diseases that result from muscle developmental defects, cardiomyopathy, and hereditary sensory neuropathy type 1 and the sphingolipidoses. Thus, the compositions of the present invention may be used to inhibit the development of cancer, metastasis, or both development of cancer and metastasis in an individual afflicted with a cancer. The compositions of the present invention may also be used in the treatment of inflammatory and immune disorders. In further embodiments, the compositions of the present invention may be used as antithrombotic therapy, such as for the therapy of pathologic thrombus

formation associated with ischemic heart disease, stroke, vascular disease, angioplasty, and stent deployment.

The compositions of the present invention may be administered to an individual afflicted with a disease associated with altered sphingolipid metabolism and/or signaling. For *in vivo* use for the treatment of human disease, an agent that modulates a component of sphingolipid metabolism and/or signaling and/or a sphingolipid intermediate as described herein is generally incorporated into a pharmaceutical composition prior to administration. A pharmaceutical composition comprises one or more modulating agents in combination with a physiologically acceptable carrier or excipient. To prepare a pharmaceutical composition, an effective amount of one or more modulating agents is mixed with any pharmaceutical carrier(s) or excipient known to those skilled in the art to be suitable for the particular mode of administration. A pharmaceutical carrier may be liquid, semi-liquid or solid. Solutions or suspensions used for parenteral, intradermal, subcutaneous or topical application may include, for example, a sterile diluent (such as water), saline solution, fixed oil, polyethylene glycol, glycerin, propylene glycol or other synthetic solvent; antimicrobial agents (such as benzyl alcohol and methyl parabens); antioxidants (such as ascorbic acid and sodium bisulfite) and chelating agents (such as ethylenediaminetetraacetic acid (EDTA)); buffers (such as acetates, citrates and phosphates). If administered intravenously, suitable carriers include physiological saline or phosphate buffered saline (PBS), and solutions containing thickening and solubilizing agents, such as glucose, polyethylene glycol, polypropylene glycol and mixtures thereof. In addition, other pharmaceutically active ingredients (including other anti-cancer agents) and/or suitable excipients such as salts, buffers and stabilizers may, but need not, be present within the composition.

A modulating agent may be prepared with carriers that protect it against rapid elimination from the body, such as time release formulations or coatings. Such carriers include controlled release formulations, such as, but not

limited to, implants and microencapsulated delivery systems, and biodegradable, biocompatible polymers, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, polyorthoesters, polylactic acid and others known to those of ordinary skill in the art.

Administration may be achieved by a variety of different routes, including oral, parenteral, nasal, intravenous, intradermal, subcutaneous or topical. Preferred modes of administration depend upon the nature of the condition to be treated or prevented. An amount that, following administration, inhibits, prevents or delays the progression and/or metastasis of a cancer is considered effective. Preferably, the amount administered is sufficient to result in regression, as indicated by 50% mass or by scan dimensions. The precise dosage and duration of treatment is a function of the disease being treated and may be determined empirically using known testing protocols or by testing the compositions in model systems known in the art and extrapolating therefrom. Controlled clinical trials may also be performed. Dosages may also vary with the severity of the condition to be alleviated. A pharmaceutical composition is generally formulated and administered to exert a therapeutically useful effect while minimizing undesirable side effects. The composition may be administered one time, or may be divided into a number of smaller doses to be administered at intervals of time. For any particular subject, specific dosage regimens may be adjusted over time according to the individual need.

In certain embodiments, particularly where the modulating agent comprises a polynucleotide, a polynucleotide encoding a modulating agent may be administered. Such a polynucleotide may be present in a pharmaceutical composition within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid, bacterial and viral expression systems, and colloidal dispersion systems such as liposomes. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal, as described above).

The DNA may also be "naked," as described, for example, in Ulmer et al., *Science 259*:1745-49, 1993.

Various viral vectors that can be used to introduce a nucleic acid sequence into the targeted patient's cells include, but are not limited to, vaccinia or other pox virus, herpes virus, retrovirus, or adenovirus. Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. Another delivery system for polynucleotides is a colloidal dispersion system. Colloidal dispersion systems include macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. The preparation and use of liposomes is well known to those of ordinary skill in the art.

Within certain aspects of the present invention, one or more modulating agents may be used to modulate expression and/or activity of a component of a sphingolipid metabolic and/or signaling pathway, in a cell or in a mammal. *In vitro*, a polypeptide that is involved in sphingolipid metabolism may be contacted with a modulating agent that increases or decreases it's activity (*e.g.,* certain antibodies, chemicals, or small molecules). In one embodiment, activity can be measured through levels of sphingolipid intermediates using assays as described herein. In a further embodiment, the modulating agent increases or decreases activity of a component of sphingolipid metabolism and/or signaling and can be assayed using methods as described herein. For use within a cell or a mammal, such modulation may be achieved by contacting a target cell with an effective amount of a modulating agent, as described herein. Administration to a mammal may generally be achieved as described herein.

As noted above, altered expression and/or activity provides a method for inhibiting the growth (*i.e.,* proliferation) of a cancer cell, either in culture or in a mammal afflicted with cancer. *In vivo*, such alteration or modulation may also be used to inhibit cancer development, progression and/or metastasis. Accordingly, one or more modulating agents as provided herein may be administered as

described above to a mammal in need of anti-cancer therapy. Patients that may benefit from administration of a modulating agent are those afflicted with cancer. Such patients may be identified based on standard criteria that are well known in the art. Within preferred embodiments, a patient is afflicted with breast cancer, as identified based on tissue biopsy and microscopic evaluation, using techniques well known in the art. In particular, patients whose tumor cells contain a tissue-specific deletion and/or alteration within an endogenous gene encoding a component of a sphingolipid metabolic and/or signaling pathway may benefit from administration of a modulating agent, as provided herein. In further embodiments, the patient may be afflicted with cancer of the breast, uterus, stomach, ovary, lung, kidney and rectum.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

Materials and Methods used in some of the Examples below are described herein as follows. (see also D. Herr, H. Fyrst, et al. 2003, Development).

Saccharomyces cerevisiae Strains and Growth Conditions

Wild type yeast used herein were of strain JK9-3d (*leu2-3,112 ura3-52 rme1 trp1 his4 HML***a**) (Heitman, J., Movva, N. R., Hiestand, P. C. and Hall, M. N. (1991). FK 506-binding protein proline rotamase is a target for the immunosuppressive agent FK 506 in Saccharomyces cerevisiae. *Proc Natl Acad Sci U S A* **88**, 1948-52.) The yeast strain JSK386 (*dpl1Δ*) is an isogenic derivative of strain JK9-3d in which the *DPL1* gene has been replaced by a G418-resistant marker (Kim, S., Fyrst, H. and Saba, J. (2000). Accumulation of phosphorylated sphingoid long chain bases results in cell growth inhibition in Saccharomyces

cerevisiae. *Genetics* **156**, 1519-29.). Strains JS204 and JS205 are derivatives of JSK386 which contain the *Drosophila melanogaster* ESTs LP04413 and GH3783 respectively in expression vector, pYES2 (Invitrogen, Inc., Carlsbad, CA). pYES2 is a yeast expression vector containing the *URA3* gene (which provides transformants the ability to grow in media without uracil), and an Ampicillin resistance marker and origin of replication functional in *Escherischia coli*. Genes expressed using this system are regulated under the control of the *GAL1,10* promoter, which allows expression in the presence of galactose and not in the presence of glucose. Cells were grown in minimal or uracil$^-$ media containing either 20g glucose or galactose per liter, as indicated.

Functional Complementation in Yeast

Strains of interest were grown to saturation in liquid culture for 2-3 days. They were then resuspended in minimal medium, placed in the first row of a 96-well plate and diluted serially from 1:2 to 1:4000 across the plate. The cultures were normalized for $O.D._{600} = 2$ and template inoculated onto a control plate and a plate containing 50 μM sphingosine, obtained from Sigma Chemical Company (St. Louis, MO). Sphingosine enriched plates were made with minimal media containing 0.0015% NP40 and 50 μM D-*erythro*-sphingosine. At this concentration of NP40, no effects on cell viability are observed. Plates were incubated at 30^{0} C for two days and assessed visually for differences in growth.

SPL Assays

SPL assays of yeast extracts from strains expressing *Drosophila melanogaster* sequences LP04413 and GH3783 were performed as previously described using a $[^{3}H]$ labeled C_{18} dihydrosphingosine substrate, obtained from American Radiolabeled Chemicals, Inc. (St. Louis, MO) (Saba, J. D., Nara, F., Bielawska, A., Garrett, S. and Hannun, Y. A. (1997). The BST1 gene of Saccharomyces cerevisiae is the sphingosine-1-phosphate lyase. *J Biol Chem*

272, 26087-26090. Van Veldhoven, P. P. and Mannaerts, G. P. (1991). Subcellular localization and membrane topology of sphingosine-1- phosphate lyase in rat liver. *J Biol Chem* **266**, 12502-7.). In this method, SPL activity is measured by determining the conversion of radiolabeled C_{18}-dihydrosphingosine substrate to long chain aldehyde product. To assess the ability of homozygous *Sply*^{05091} versus wild type flies to degrade endogenous LCBPs, an HPLC method was developed and employed to examine extracts of wild type and homozygous *Sply*^{05091} adults. Endogenous LCBPs were first isolated as described under 'Analysis of *Drosophila melanogaster* Sphingolipids,' and the lipid extract from 15 mg of homozygous *Sply*^{05091} flies were dried down using nitrogen gas. Lipids were resuspended in SPL reaction buffer and incubated for various time points @ 37°C. Lipids were reisolated, derivatized with *o*-phthalaldehyde and analyzed by HPLC, as described below. Activity was determined by measuring the percent degradation of endogenous LCBPs in comparison to standards incubated in the absence of protein extracts.

<u>Developmental Expression of *Sply*</u>

For Northern analysis, full-length probes were labeled by random priming with [γ-^{32}P] dGTP. Hybridization was carried out under standard conditions against an RNA blot prepared from total RNA of flies harvested at different stages of development (embryos at hours 0-4, 4-8, 8-12, 12-24, larval instars 1st, 2nd, 3rd and adults). *RpL32* is a constitutively expressed ribosomal gene used as a loading control.

In situ hybridization was performed with a digoxygenin-labeled probe (Roche cat# 1 175 025) and hybridized to fixed embryos at various stages essentially as described (Tautz, D. and Pfeifle, C. (1989). *Chromosoma* **98**, 81-5.).

Analysis of *Drosophila* sphingolipids

100 mg of flies were homogenized in 6 ml of ice cold methanol/water 1:1 (vol: vol) with a Potter-Elvehjem homogenizer with a loose pestle followed by a tight pestle until the pestle moved smoothly. Extract was further homogenized by tip sonication for 3 times 20 sec. Extract was spun at low speed and supernatant was removed and dried down in speed vac. Extract was resuspended in 500 µl of methanol containing 0.1M ammonium hydroxide and incubated for 1 hour at 37° C. Following incubation the extract was dried down in speed vac. Extract was resuspended in 500 µl of 50% methanol containing 0.1% glacial acetic acid and applied to a C18E STRATA solid phase extraction column. C18E STRATA column was washed with 50% methanol containing 0.1% glacial acetic acid followed by a wash with 100% methanol containing 0.1% glacial acetic acid. Lipids of interest were eluted with methanol/10 mM ammonium acetate, 9:1 (vol: vol). Lipids were dried down in speed vac. and *o*-pthaladehyde labeled for HPLC analysis as previously described (Kim, S., Fyrst, H. and Saba, J. (2000). *Genetics* 156, 1519-29.).

Lethal Phase Analysis

100 embryos from the indicated lines were collected and observed at each developmental stage. Viability is expressed as the percentage of flies that survived through the indicated stage.

Adult Flight Performance

2-7 day old adult flies were released into a top-lit Plexiglas chamber. Flight behavior was scored as follows: upward flight = 3, lateral flight = 2, downward flight = 1, flightless = 0 (Vigoreaux, et al., 1993 J. Cell Biol. May; 121(3):587-98). Average flight scores were compared using a two-tailed student t-test.

Adult and Larval Microscopy

Preparation of tissue, staining, mounting and visualization was performed using standard techniques (Sullivan, W., Ashburner, M. and Hawley, R. S. (2000). Drosophila protocols. Cold Spring Harbor, N.Y.: Cold Spring Harbor Laboratory Press.). Thoraces from adult flies were dissected, fixed with formaldehyde and osmium tetroxide, and embedded in EPON. These blocks were then cut into 1 μm thick sections, stained with methylene blue and azure II, and visualized with a Lieca DMIRBE microscope.

Larvae were filleted during the third instar, pinned with the dorsal cuticle down, and eviscerated to allow an unobstructed view of the body wall muscles. The tissue was fixed with 4% formaldehyde, permeabilized in 100% acetone, and stained with fluorescein-conjugated phalloidin. (Molecular Probes cat# F-432).

Electron microscopic analysis of DLMs was performed on adults essentially as described (O'Donnell, P. T. and Bernstein, S. I. (1988). *J Cell Biol* **107**, 2601-12.).

Hemithoraces were visualized essentially as described (Fyrberg, E. A., Bernstein, S. I. and VijayRaghavan, K. (1994). *Methods Cell Biol* **44**, 237-58.). Briefly, adult flies were frozen in liquid nitrogen, bisected with a razor blade, and dehydrated in an ethanol series. The cuticles were then cleared with methyl salicylate to allow visualization of the muscles with a Lieca DMIRBE microscope under polarized light.

Fluorescent Microscopy

0-24 hour embryos were prepared and fixed using standard techniques (Rubin Manual) and stained with the indicated primary antibody or assayed for apoptosis using a TUNEL-based staining method (In situ cell death detection kit, Roche 1 684 795). Incorporation of fluorescein was assessed with a

Leica DMIRBE epifluorescence microscope and an upright Leica TCS-NT confocal laser scanning microscope.

Antibodies and fluorescent reagents were as follows: polyclonal rabbit anti-*Drosophila* myosin heavy chain (Kiehart, D. P. and Feghali, R. (1986). Cytoplasmic myosin from *Drosophila melanogaster*. *J Cell Biol* **103**, 1517-25.) 1:1,000. Polyclonal rabbit anti-DMEF2 (Lilly et al., 1995) 1:10,000. Secondary antibody was a fluorescein-conjugated goat anti-rabbit IgG (Jackson ImmunoResearch Laboratories, Inc.) 1:1,000.

<u>Genetics</u>

The precise excision of the ry^+ PZ P-element was performed by introducing transposase allele Δ2-3 into insertion line BL-11393. In the subsequent generation the transposase was removed and the second chromosome was balanced over CyO. Offspring of these flies that lacked the P-element were selected by scoring for loss of ry^+. Homozygous lines were generated, assayed for restoration of flight behavior, and assessed for precise excision by PCR if indicated. Lines homozygous for the $Sply^{05091}$ allele the $lace^{k05305}$ allele were generated by meiotic recombination. $Sply^{05091}$and $lace^{k05305}$ mutations were introduced in trans and balanced in the next generation. Flies carrying the $lace^{k05305}$ allele were selected by presence of w^+. Presence of $Sply^{05091}$ was verified by PCR.

<u>Preparation of Transgenic *Drosophila melanogaster*</u>

Relevant methods of preparing transgenic *Drosophila melanogaster* are disclosed in: Spradling, A. C., and Rubin, G. M. (1982). Science 218, 341-347; Brand & Perrimon, Development (1993) 118: 401-415; and Phelps & Brand, Methods (April 1998) 14:367-379. See also, Spradling A C, P Element Mediated Transformation in Drosophila: A Practical Approach (ed. D. D. Roberts, IRL Press, Oxford)(1986) pp 175-179.

Generally, *Drosophila melanogaster* stocks used in the experiments described herein are as follows: Wild type Canton-S (BL-1), *Sply*^{05091} (BL-11393), *lace*^{2} (BL-3156) and *lace*^{k05305} (BL-12176) lines, obtained from the Bloomington *Drosophila* Stock Center (Indiana University, Bloomington, IN). General fly husbandry was performed as described (Sullivan, W., Ashburner, M. and Hawley, R. S. (2000). Drosophila protocols. Cold Spring Harbor, N.Y.: Cold Spring Harbor Laboratory Press).

Other techniques useful in generating mutant and/or transgenic flies are described in Rubin, G, Hong L, Brokstein P, Evans-Holm M, Frise E, Stapleton M and Harvey D, 2000. A *Drosophila* complementary DNA resource, *Science* 287:2222-2224.

EXAMPLE 1

ISOLATION AND CHARACTERIZATION OF SPL cDNA FROM *DROSOPHILA MELANOGASTER* (*SPLY*)

In order to seek out the *Drosophila melanogaster* SPL cDNA and genomic sequence, the *D. melanogaster* genomic database was searched for sequences which demonstrated significant homology to human SPL cDNA. The *Drosophila melanogaster* genomic database (http://flybase.bio.indiana.edu) was searched for predicted proteins using mouse (accession number AAH26135; amino acid sequence set forth in SEQ ID NO:6) and human (accession number XP_166113; amino acid sequence set forth in SEQ ID NO:18) SPL sequences. DNA homology searches were performed via the Berkeley *Drosophila* Genome Project web site using the BLAST search program (http://www.ncbi.nlm.nih.gov). One computed gene (CG8946) was identified that corresponded to a predicted SPL gene. Subsequently, two ESTs (LP04413, cDNA set forth in SEQ ID NO:27 and GH13783, cDNA set forth in SEQ ID NO:26) were identified which contained open reading frames that corresponded to the two predicted splice variants. The

two clones are predicted based on alternative 5' exon usage and may be expressed in different subcellular locations.

The predicted *Drosophila melanogaster* SPL is located on the right arm of chromosome II, position 53F8-12. The cDNA sequence for the coding region of the *Drosophila melanogaster* SPL is set forth in SEQ ID NO:15 and encodes the SPL protein set forth in SEQ ID NO:16. The *Drosophila* SPL predicted protein sequence set forth in SEQ ID NO:16 is 49%, 49% and 43% identical to human, mouse and yeast SPL protein sequences, respectively.

In order to evaluate whether these clones contained a functional SPL gene, they were recloned into the yeast expression vector, pYES2 in which gene expression is driven by a galactose-inducible promoter. The open reading frame contained in LP04413 (polynucleotide sequence set forth in SEQ ID NO:) was amplified using primers LPEcoRI5 = 5′-TGGAATTCGATGCGTCCGTTCTCCGGCAGC-3′ and LPXhoI3′ = 5′-CTCCTCGAGTCTATTTCTGGCTGGGAGT-3′ and was cloned into the yeast expression vector, pYES2, at *Eco*RI and *Xho*I restriction sites. This construct was transformed into a *dpl1Δ* strain using the lithium acetate method (Itö, H., Fukuda, Y., Murata, K. and Kimura, A. (1983). *J Bacteriol* 153, 163-8.). These constructs were transformed into a *dpl1Δ* strain in which the sole endogenous Saccharomyces cerevisiae SPL gene has been deleted (Saba, J. D., Nara, F., Bielawska, A., Garrett, S. and Hannun, Y. A. (1997). *J Biol Chem* **272**, 26087-26090.). The *dpl1Δ* strain is unable to catabolize LCBPs, and it cannot proliferate on media containing low concentrations of D-*erythro*-sphingosine.

Expression of clones containing the potential *Drosophila melanogaster* SPL fully complement the *dpl1Δ* strain's sensitivity to 50 μM D-*erythro*-sphingosine. Further, whole cell extracts of *dpl1* strains containing either pYES2-LP04413 or pYES2-GH3783 demonstrate restoration of SPL enzyme activity to wild type levels or greater, although not as high as a *DPL1*

overexpressing strain (DPL OE). Further, whole cell extracts of *dpl1Δ* strains overexpressing *Sply* demonstrate restoration of SPL enzyme activity.

Northern analysis of wild type *Drosophila melanogaster* embryos and larvae indicates that *Sply* expression is developmentally regulated, with the onset of expression occurring by 8-12 hours of embryogenesis. Embryonic expression was largely localized to the gut primordium as indicated by *in situ* hybridization.

Thus, this example describes *Sply,* the sphingosine-1-phosphate lyase gene in *Drosophila melanogaster.*

EXAMPLE 2

GENERATION AND CHARACTERIZATION OF SPL TRANSPOSON MUTANT *D. MELANOGASTER*

Drosophila melanogaster stocks used in the experiments described herein are as follows: Wild type Canton-S (BL-1), *Sply*^{05091} (BL-11393), *lace*^{2} (BL-3156) and *lace*^{k05305} (BL-12176) lines, obtained from the Bloomington *Drosophila* Stock Center (Indiana University, Bloomington, IN). General fly husbandry was performed as described (Sullivan, W., Ashburner, M. and Hawley, R. S. (2000). Drosophila protocols. Cold Spring Harbor, N.Y.: Cold Spring Harbor Laboratory Press)

Flies from the Berkeley *Drosophila* Genome Project gene disruption project (Spradling, A. C., Stern, D. M., Kiss, I., Roote, J., Laverty, T. and Rubin, G. M. (1995). Gene disruptions using P transposable elements: an integral component of the Drosophila genome project. *Proc Natl Acad Sci U S A* **92**, 10824-30.) were identified that harbor a transposon within the *Sply* open reading frame (designated Sply^{05091}). The transposon is located at nucleotide +269 relative to the start site of the larger transcript, LP04413, cDNA set forth in SEQ ID NO:27.

These flies were genetically crossed using techniques well known to ordinarily skilled artisans, and progeny were evaluated for the presence of homozygous insertional mutants (based on presence of rosy eye color, encoded

by a recessive marker carried on the P-element). Northern analysis of total RNA obtained from *Sply*^{05091} homozygotes confirmed an absence of *Sply* expression.

To determine the SPL function of each genotype, +/+, +/- and -/- flies were homogenized and whole extracts assayed for SPL activity. It was observed that SPL genotype corresponded with SPL activity with +/+ > +/- > -/-. Initial evaluation of homozygous mutants indicated that adult SPL mutants were flightless, suggesting a potential defect in either muscle development or energetics of the adult fly. Flight analysis was carried out essentially as described (Vigoreaux, J., J. Saide, K. Valgeirdottir, and M. Pardue. 1993. Flightin, a novel myofibrillar protein of *Drosophila* stretch-activated muscles. *J Cell Biol.* 121:587-598) by determining the percentage of flies that were flightless or exhibited downward, upward, or lateral flight capabilities in control Canton-S flies as compared to mutant flies as follows: 2-7 day old adult flies were released into a top-lit Plexiglas chamber. Flight behavior was scored as follows: upward flight = 3, lateral flight = 2, downward flight = 1, flightless = 0 (Vigoreaux, et al., 1993). Average flight scores were compared using a two-tailed student t-test.

EXAMPLE 3

FURTHER CHARACTERIZATION OF THE *SPLY* P-ELEMENT INSERTIONAL MUTANT *DROSOPHILA MELANOGASTER*

The sphingolipids of *Drosophila melanogaster* contain C_{14} and C_{16} sphingosine and dihydrosphingosine LCBs (see Example 4). Extracts of wild type and mutant flies were compared for their ability to degrade endogenous *Drosophila melanogaster* LCBPs in vitro. Extracts of *Sply*^{05091} mutants failed to catabolize endogenous LCBPs, whereas extracts of wild type flies degraded endogenous *Drosophila melanogaster* LCBPs, indicating that the *Sply* gene product is responsible for LCBP catabolism in this organism.

To determine whether loss of *Sply* expression affects the levels of *Drosophila melanogaster* endogenous LCBs and corresponding LCBPs, the

sphingolipid profile of homozygous *Sply*^{05091} flies was evaluated and compared to wild type controls. Homozygous *Sply*^{05091} adults demonstrated an eight-fold increase in LCBs and a 20-fold increase in LCBPs when compared to wild type (Table 1), indicating significant derangement of sphingolipid metabolism. This accumulation of LCBs and LCBPs was observed in homozygous *Sply*^{05091} mutants as early as hours 12-18 of embryogenesis, correlating with the onset of *Sply* expression.

<u>Table 1</u>

<u>Biochemical and Biological Characteristics of Mutant Models of Sphingolipid Metabolism</u>

A. Characteristic	Canton-S	*Sply*^{05091}	*Sply*^{14a}	*lace*$^{k05305/2}$	*lace*$^{k05305/+}$, *Sply*^{05091}	*lace*^{k05305}, *Sply*^{05091}	*Sply*^{05091}+1 mM D,L-*threo*-DHS
$C_{14/16}$ LCBs (nmol/100 mg)	2.71 ± 0.28	24.22 ± 1.73	5.30 ± 0.59	0.15 ± 0.01	12.67 ± 1.93	5.75 ± 0.42	136% *
$C_{14/16}$ LCBPs (nmol/100 mg)	0.30 ± 0.09	6.38 ± 0.44	1.02 ± 0.33	0.08 ± 0.04	4.06 ± 0.64	1.88 ± 0.17	81% *
Average flight score	2.60 ± 0.032	0.40 ± 0.036	1.70 ± 0.074	1.62 ± 0.14	1.41 ± 0.063	0.56 ± 0.13	0.62 ± 0.057
# of DLM fibers/hemithorax	6.00 ± 0.00	4.15 ± 0.21	5.97 ± 0.089	5.94 ± 0.030	5.13 ± 0.26	5.81 ± 0.14	N.D.
Average # of eggs/day	44.5 ± 3.28	15.8 ± 2.98	43.4 ± 3.43	N/A	52.9 ± 4.03	N/A	N.D.
Developmental lethality	20%	66.5%	27%	N.D.	20%	N.D.	N.D.

Adult wild type flies and the indicated models of sphingolipid metabolism were analyzed for total phosphorylated (LCBPs) and unphosphorylated (LCBs) long chain base levels, flight performance, number of DLM per hemithorax, fecundity (egg-laying), and % mortality prior to completion of metamorphosis. Flight performance and LCB/LCBP levels were also determined in *Sply*^{05091} homozygous flies treated with the sphingosine kinase inhibitor, D,L-*threo*-DHS. LCB/LCBP levels in inhibitor-treated flies are given as percentage of untreated controls; these determinations were obtained in a separate experiment, and baseline sphingolipid levels were not comparable between the two experiments. Canton-S is wild type. *Sply*^{05091} indicates the homozygous *Sply* null mutant. *lace*^{2} and *lace*^{k05305} are recessive lethal alleles of serine palmitoyltransferase. *Sply*^{14a} indicates the homozygous *Sply*^{05091} revertant. All biochemical, flight, and fiber count data were obtained from mixed-age adults. Values are as indicated, ±s.e.m.

Homozygous and heterozygous *Sply*^{05091} flies were examined for evidence of anatomical, developmental, and functional abnormalities. Flies

heterozygous for *Sply*^{05091} were indistinguishable from wild type. Initial evaluation of flies homozygous for the *Sply*^{05091} allele revealed no obvious defects in external anatomical structures at embryonic, larval or adult stages. However, adult mutants were almost uniformly flightless, with 91% of the mutant population scoring zero (in comparison to 4% wild type flies) in a standard flight performance assay (Table 1). Despite the severity of the flight defect in *Sply*^{05091} homozygotes, the function of other muscle groups, including the jump and leg muscles did not appear to be affected. Moreover, evaluation of the giant fiber neuromuscular pathway by electrophysiological analysis indicated that this pathway remained functionally intact and was not responsible for the observed flight defect.

<u>*Sply*^{05091} Homozygotes Demonstrate Abnormal Flight Muscle Morphology.</u>

To investigate further the etiology of *Sply*^{05091} flight defects, adult mutants were sectioned through the thoracic region, and muscles were examined by light microscopy.

These studies revealed a reduction in the number of muscle fibers comprising the DLMs required for flight. Whereas the thoraces of wild type flies invariably contained 6 symmetrical pairs of fibers, *Sply*^{05091} homozygotes exhibited a general pattern of missing fibers, asymmetry, and hypertrophy of remaining fibers. Quantitative analysis of DLM fibers revealed a reduction from 6 per hemithorax in wild type to an average of 4.15 per hemithorax in the mutants (Table 1). Microscopic analysis of hemithoraces illuminated with polarized light confirmed the abnormal muscle configuration while demonstrating that muscle insertions were not affected.

<u>*Sply*^{05091} Mutation Does Not Disrupt Muscle Ultrastructure, Template Formation or Embryonic Muscle Fusion</u>

To determine the origin of the DLM defect, adult myocyte ultrastructure and larval and embryonic muscle development were investigated.

Examination of Dmef2 expression in myoblast nuclei of nascent muscle fibers of early wild type and mutant embryos revealed no appreciable differences in muscle organization. Thus, myoblasts appear to successfully migrate from somites to correct sites in mutant embryonic segments. Similarly, analysis of myosin heavy chain expression in 0-24 hour wild type and mutant embryos revealed no gross changes in the organization of the developing mutant muscle fibers as compared to wild type indicating that myocyte fusion was not impaired.

To determine whether the DLM defect observed in *Sply*^{05091} adult homozygotes occurred due to lack of template structures required for their formation during metamorphosis, T2 dorsal oblique muscles (DOMs) were evaluated in mutant larvae. Late-stage mutant larvae exhibited no alterations in number and/or size of DOMs. Therefore, it appears that the mutant muscle defect is restricted to DLMs and affects the adult muscle configuration subsequent to myoblast fusion events during metamorphosis. Despite this defect, the ultrastructure of the DLMs that are present in the *Sply*^{05091} mutants generally appear to be intact as evidenced by transmission electron microscopy.

<u>*Sply*^{05091} Homozygotes Demonstrate Decreased Fecundity, Semi-Lethality and Increased Apoptosis in Embryos</u>

The number of offspring resulting from homozygous *Sply*^{05091} crosses was about 10% of the number observed in wild type crosses. This loss of progeny could result from diminished egg-laying and/or diminished survival of embryos and larvae. Analysis of egg-laying indicated that fecundity of the mutants was about one third that of control flies (Table 1). This outcome could be the result of diminished male and/or female fertility. To distinguish between these possibilities, both male and female *Sply*^{05091} homozygotes were mated to wild type flies, and egg-laying was measured in comparison to wild type pairs and homozygous mutant pairs. Numbers of eggs produced were significantly diminished in crosses of both male and female mutant flies with wild type mates

(data not shown), indicating that the effect on fecundity was not gender-specific. Additionally, crosses between *Sply*^{05091} homozygous males and females resulted in progeny with an overall survival (from egg to adulthood) of 33.5%, compared to an 80% survival rate in wild type flies. Lethality in the *Sply*^{05091} mutants was high during larval stages (46%, compared to 3% in wild type), with the majority of larval death occurring during the first larval instar. Less severe effects were observed during pupation (22% lethality, compared to 1% in wild type), and no appreciable differences in survival were noted during embryogenesis. *Sply*^{05091} mutant embryos were examined by in situ TUNEL assay, and patterns of apoptosis were compared to those of wild type controls. *Sply*^{05091} mutant embryos demonstrated a pronounced enhancement of apoptosis compared to wild type controls, especially in a specific region of the posterior pole near the developing genital disc.

EXAMPLE 4

CHARACTERIZATION OF SPHINGOLIPID SPECIES IN THE *DROSOPHILA MELANOGASTER*

Without being bound by theory, it is hypothesized that the phenotype of the SPL mutant *Drosophila melanogaster* is caused by an abnormal level of S-1-P during development. Further, without being bound by theory, it is our hypothesis that phosphorylated sphingoid base species are responsible for regulating cell proliferation, migration and other events required for both tumor formation and normal developmental processes in this model organism. Therefore, characterization of sphingolipid species in *Drosophila melanogaster* was determined.

<u>Method</u>

Wild type (Canton S) whole fly extracts were prepared by mechanical disruption. Lipids were isolated by two-phase extraction and derivatized with the fluorescent molecule o-pthalaldehyde essentially as described in Caligan, et al. hereby incorporated by reference in its entirety (Caligan, T.B., K. Peters, J. Ou, E.

Wang, J. Saba, and A.H. Merrill, Jr. 2000. A high-performance liquid chromatographic method to measure sphingosine 1-phosphate and related compounds from sphingosine kinase assays and other biological samples. *Analytical Biochemistry.* 281:36-44). Derivatized lipid extracts were separated by HPLC using a C_{18} ODS column (LUNA 4.6 x 250 mm) and mobile phase MeOH/$H_2$0/1M TBAP 82:17:0.9, pH 4.8. Standards included commercially available C_{10}, C_{12}, C_{14}, C_{16}, C_{18} and C_{20} sphingosines, as well as the phosphorylated forms of these standards, prepared by incubation of sphingosine standards with extract from a yeast strain which overexpresses the major yeast sphingosine kinase, *LCB4*.

<u>Results</u>

Drosophila melanogaster extracts contained only sphingolipid species which comigrated with C_{14} sphingosine and C_{14} sphingosine-1-phosphate (S-1-P) standards under the stated conditions. To verify the identity of the peaks in fly extracts which comigrated with C_{14} sphingosine and C_{14}S-1-P standards, extracts and standards were compared in four different mobile phase buffers. The peak identified as C_{14} sphingosine comigrated with the C_{14} sphingosine standard under all four conditions (Table 2). However, the peak identified as C_{14}S-1-P demonstrated a slight difference from the C_{14}S-1-P standard under conditions which exploit differences in charge (MeOH/10 mM KP/1 M TBAP, pH 7.2, 81:18:1).

Table 2

Sphingolipid Identification

Mobile Phase	$C_{14}S$ std	$C_{14}S$ in extract	$C_{14}S$-1-P std	$C_{14}S$-1-P in extract
MeOH/$H_2$0/1M TBAP pH 4.8 82.1:17:0.9	19.1 min	19.0 min	14.8 min	14.8 min
MeOH/$H_2$0/1M TBAP pH 4.8 79.1:20:0.9	27.3 min	27.1 min	22.5 min	22.1 min
MeOH/10mM KP/ 1M TBAP pH 5.5 81:18.1	21.9 min	22.0 min	18.3 min	17.2 min
MeOH/10mM KP/ 1M TBAP pH 7.2 81:18.1	21.4 min	21.8 min	15.0 min	17.1 min

This finding is likely to be due to a chemical modification of the phosphate group, since a phosphatase capable of dephosphorylating the $C_{14}S$-1-P standard does not recognize this substrate. Mass spectroscopy is being utilized to identify the phosphate group modification of this S-1-P species. Herein, this sphingolipid is referred to as "modified $C_{14}S$-1-P."

EXAMPLE 5

GENETIC REVERSION OF THE *SPLY*^{05091} MUTATION RESTORES NORMAL MUSCLE CONFIGURATION

To verify the importance of *Sply* in mediating the semi-lethality, egg-laying defects and flight muscle phenotype of the mutant line, the transposon in the *Sply*^{05091} locus was mobilized Genetic reversion of the *Sply*^{05091} mutation restores normal muscle configuration. in *Sply*^{05091} homozygotes following introduction of an active transposase. Precise excision of the transposon was subsequently confirmed by PCR and DNA sequence analysis. A homozygous revertant line (*Sply*^{14a}) was generated as described in Materials and Methods and

was found to express *Sply* mRNA at levels equivalent to wild type. *Sply*^{14a} demonstrated reversion of the muscle fiber morphology defect, and flight performance was largely restored (Table 1). Additionally, apoptosis in the revertant embryo was diminished in comparison to *Sply* mutants. The appearance of the specific cluster of TUNEL-positive cells was <1% (n=197), 48% (n=160) and 72% (n=324) in Canton-S, *Sply*^{14a}, and *Sply*^{05091} in stage 12-15 embryos, respectively. Phenotypic reversion correlated with normalization of LCB and LCBP levels in revertant extracts (Table 1).

EXAMPLE 6

THE *SPLY*^{05091} MUSCLE DEFECT IS SUPPRESSED BY REDUCING SPHINGOLIPID INTERMEDIATES

To investigate the possibility that the *Sply*^{05091} muscle phenotype was caused by accumulation of LCBPs, an inhibitor of sphingosine kinase, D,L-*threo*-DHS, was introduced to the growth media of mutant and wild type flies. Flies were grown on the supplemented media, and F2 progeny were examined. When wild type flies were grown on media supplemented with 10 μM D,L-*threo*-DHS, no deleterious effects were observed. *Sply*^{05091} mutants grown on this media demonstrated a slight but significant improvement in flight performance. To determine whether the flight improvement coincided with a restoration of LCBP levels, LCB/LCBP levels were analyzed in mutants and controls grown on D,L-*threo*-DHS. LCBP levels in *Sply*^{05091} homozygotes grown in the presence of sphingosine kinase inhibitor were reduced by approximately 20% (Table 1). Similarly, LCBP levels in wild type flies were reduced to 20% of normal levels.

Assuming that the mutant phenotypes are caused by an accumulation of LCB/LCBPs, we predicted that diminishing SPT activity in the *Sply*^{05091} homozygote would suppress the *Sply*^{05091} phenotype by reducing production of sphingolipid intermediates. Toward that end, a *lace*^{k05305} null allele was introduced onto the *Sply*^{05091} chromosome by genetic recombination, thus

generating a *Sply*^{05091}, *lace*^{k05305}/+ line. *Sply*^{05091}, *lace*^{k05305}/*Sply*^{05091}, *lace*$^{+}$ flies exhibited reversion of the abnormal muscle patterning, and flight performance was substantially improved (Table 1). Additionally, the pattern of embryonic apoptosis appeared similar to that of the wild type. Phenotypic reversion correlated with a marked reduction of the LCBs and LCBPs (Table 1).

EXAMPLE 7

LOSS OF *SPLY* EXPRESSION SUPPRESSES THE *LACE* NULL PHENOTYPE.

Inheritance of two *lace*^{k05305} hypomorphic alleles was reported to be almost completely lethal, whereas a heterozygous allelic combination (*lace*^{k05305}/*lace*^{2}) yields flies that frequently survive but manifest severe developmental phenotypes leading to eye, bristle and wing abnormalities (Adachi-Yamada, T., Gotoh, T., Sugimura, I., Tateno, M., Nishida, Y., Onuki, T. and Date, H. (1999). *Mol Cell Biol* **19**, 7276-7286.). We predicted that the *lace* mutant phenotype is due to diminished levels of sphingolipid intermediates. Further, we reasoned that inhibiting sphingolipid catabolism in *lace* mutants might allow sufficient accumulation of trace sphingolipids obtained through the diet to ameliorate developmental defects induced by the lack of critical sphingolipid intermediates. To address this possibility, a *Drosophila melanogaster* line homozygous for both the *Sply*^{05091} and *lace*^{k05305} alleles was generated. Significantly, the presence of the *Sply*^{05091} allele increased the recovery of *lace* homozygotes from 9% to 39% of that expected by independent assortment. Furthermore, the introduction of *Sply*^{05091} fully suppressed the eye, bristle and wing phenotypes in the resulting flies. In accordance, sphingolipid intermediates were substantially increased in this line, in comparison to *lace*^{2}/*lace*^{k05305} heterozygotes, which are the only available *lace* mutants with sufficient viability for comparison (Table 1).

EXAMPLE 8

HUMAN SPL AND SK EXPRESSION PATTERNS IN CANCER

To determine if SK and/or SPL expression is altered in human tumors, we utilized a cancer profiling array which contains more than 240 cDNA pairs representing tumor tissue and corresponding normal tissue from the same patient. By utilizing tissue pairs from one patient, differences between gene expression in tumor and normal tissue which might be due to person to person variability should not confound the interpretation of results. Additionally, each blot was normalized for loading using four separate housekeeping genes.

Standard hybridization techniques known in the art were utilized to probe this cDNA blot with the full length human SPHK1 cDNA (set forth in SEQ ID NO:22), which was obtained by RT-PCR of human umbilical vein endothelial cell total RNA. Analysis of the array indicates that SK expression appears to be significantly increased in numerous human cancers including tumors of breast, uterus, stomach, ovary, lung, kidney and rectum. Additionally, some tumors demonstrated increased SK expression in metastatic lesions compared to tumor tissues. None of the SK overexpressing tumors demonstrate loss of SPL expression. Thus, altered SK expression is observed in primary human tumors. Therefore, modulating the activity of SK protein either by altering gene expression or through direct action on the protein may provide a useful treatment for individuals afflicted with an SK-related cancer. Furthermore, SK expression serves as a useful diagnostic marker of cancer in humans.

Standard hybridization techniques were utilized to probe the cDNA blot with a 300 nucleotide 3' fragment of human SPL cDNA (SEQ ID NO:23), which was obtained as described in U.S. Patent No. 6,423,527. Analysis of the array indicated that, whereas human SPL expression is matched closely in most tissue pairs, it is significantly reduced in colon cancer specimens, with a 50% reduction in expression in colloid cancer of the colon and 61% reduction in adenocarcinoma of the colon. Reduced SPL expression was also seen in

adenocarcinaom of the uterus. None of the tumors in which SPL expression is diminished demonstrates SK overexpression. Thus, altered SPL expression is observed in primary human tumors. Therefore, modulating the activity of SPL protein either by altering gene expression or through direct action on the protein may provide a useful treatment for individuals afflicted with an SPL-related cancer. Furthermore, SPL expression serves as a useful diagnostic marker of cancer in humans.

EXAMPLE 9

ISOLATION OF *DROSOPHILA MELANOGASTER* GENES INVOLVED IN SPHINGOLIPID METABOLISM

Drosophila melanogaster genes that are involved in sphingolipid metabolism were identified. Using the human SK protein sequence set forth in SEQ ID NO:21 as probe, we identified two homologous *Drosophila melanogaster* sequences which could potentially encode fly SK proteins. These two *Drosophila melanogaster* SK protein sequences are set forth SEQ ID NOs: 19 and 20 and are shown in Figure 1. The annotation FBan0001747 for gene CG1747, which has FlyBase accession number FBgn0030300, is located on chromosome arm X, and has a transcription unit length of 2020 nucleotides. This gene has the transcript CT5088. The function of this gene has been categorized as enzyme/diacylglycerol kinase, based upon a conserved lipid kinase domain. The annotation FBan0002159 for gene CG2159, which has FlyBase accession number FBgn0035391, is located on chromosome arm 3L, and has a transcription unit length of 4431 nucleotides. This gene has the transcript CT2650. These two sequences have not been cloned, and neither functional data nor ESTs are available. (DSK1747 amino acid sequence is set forth in SEQ ID NO:19; DSK2159 amino acid sequence is set forth in SEQ ID NO:20).

EXAMPLE 10

CHARACTERIZATION OF 2 *DROSOPHILA MELANOGASTER* SK GENES INVOLVED IN SPHINGOLIPID METABOLISM

In order to identify potential SK genes in *Drosophila melanogaster*, the *Drosophila melanogaster* genomic database was searched using a tBLASTn enquiry for sequences that demonstrated significant homology to human SK cDNA. This led to the identification of two candidate SK as described above. Gene CG1747 is located on chromosome X and has been categorized as enzyme/diacylglycerol kinase, based upon a conserved lipid kinase domain. Gene CG2159 is located on chromosome arm 3L, and has a transcription unit length of 4431 nucleotides. ESTs corresponding to these two loci were obtained, their integrity confirmed by sequence and restriction analysis (sequences of the full length amino acids of SK1 and SK2 are set forth in SEQ ID NOs:28 and 29; full length cDNAs for SK1 and SK2 are set forth in SEQ ID NOs:24 and 25). These CG1747 and CG2159 cDNA clones were then re-cloned into yeast expression vector pYES2, under regulation of a galactose-inducible promoter (Rubin, G, Hong L, Brokstein P, Evans-Holm M, Frise E, Stapleton M and Harvey D, 2000. A *Drosophila* complementary DNA resource, *Science* 287:2222-2224.). These constructs were transformed into yeast strain JSK392 (Kim, S, Fyrst H and Saba J, 2000. *Genetics* 156:1519-1529.), in which the endogenous SPL, SK and S-1-PP genes (*DPL1*, *LCB4* and *YSR2* respectively) have been deleted. This strain can survive in the absence of LCBP synthesis, but expression of a functional SK gene in this background is lethal, due to severe accumulation of LCBPs which cannot be degraded. When CG1747 and CG2159 expression was induced in this background in the presence of galactose, no yeast growth occurred, indicating that these cDNAs encode functional SK enzymes. Finally, a CG2159 transposon mutant was obtained and demonstrates lack of expression from this locus (Rosemann, R, Johnson E, Rodesch C, Bjerke M, Nagoshi R and Geyer P, 1995. *Drosophila melanogaster*, *Genetics* 141:1061-1074.). This mutant (*Sphk2*^{KG05894})

was created by the insertion of a P-element into the 5' UTR of CG2159, as previously described. Preliminary studies indicate this mutant has a mild defect in DLMs, similar to that seen in *Sply* mutants.

EXAMPLE 11

CHARACTERIZATION OF THE CHEMICAL STRUCTURES AND CONCENTRATION OF SPHINGOLIPID METABOLITES IN WILD TYPE FLIES AND THOSE WITH DEFECTS OF SPHINGOLIPID METABOLISM

Materials and Methods

Drosophila melanogaster Lines

The *lace* gene encodes one subunit of a *Drosophila* serine palmitoyltransferase. Inheritance of two *lace*^{k05305} null alleles is reported to be uniformly lethal, whereas the heterozygous allelic combination used in these experiments, *lace*^{k05305}/*lace*^{2}, leads to severe developmental phenotypes and a low percentage of viable progeny (Adachi-Yamada, T., T. Gotoh, I. Sugimura, M. Tateno, Y. Nishida, T. Onuki, and H. Date. 1999. *Mol. Cell. Biol.* 19: 7276-7286.). A *Drosophila* line homozygous for a null allele of one of two putative sphingosine kinase (SK) genes was also utilized in these experiments. This mutant (*Sphk2*^{KG05894}) was created by the insertion of a P-element into the 5' UTR of CG2159, as previously described. The product of this gene functionally complements a yeast SK mutant. Wild type Canton-S (BL-1), *lace*^{2} (BL-3156), *lace*^{k05305} (BL-12176), and *Sphk2*^{KG05894} (BL-14133) lines were obtained from the Bloomington *Drosophila* Stock Center (Indiana University, Bloomington, IN).

Flies were reared on standard fly media at room temperature. In all cases, control and mutant flies were reared in parallel under identical conditions. For developmental analysis, adult flies were allowed to deposit embryos on grape juice agar plates. After the collection period, plates were removed from the collection chamber, covered, and aged at room temperature to obtain

appropriately staged embryos. For example, to collect 6-12 hour embryos, adults were exposed to plates for 6 hours, plates were removed and aged for an additional 6 hours before embryos were collected. Embryos were removed from the plates by washing with 0.7% sodium chloride/0.03% TritonX-100, rinsed extensively with water and frozen at –70•C for storage.

Preparation of Drosophila Lipid Extracts

Samples containing 25 mg of frozen intact fly material were placed in a 7 ml Potter Elvehjem homogenizer. 20 µl of a mixture of internal LCB standards (Matreya Inc., Pleasant Gap, PA) containing 250 to 500 pmol of each LCB were then added. Flies were homogenized in 2 ml of ice cold methanol/water, 1:1 (v/v) with a loose pestle followed by a tight pestle until it moved smoothly. Extracts were further homogenized with a tip sonicator (3 x 20 sec.) while on ice, then transferred to a glass tube and centrifuged at 1500 x g for 10 minutes. Supernatants were recovered and dried down in a speed vac. Extracts were resuspended in 200 µl of methanol containing 0.1 M ammonium hydroxide, followed by vortexing, bath sonication and incubation at 37• C for 1 hr to allow hydrolysis of esterified acyl chains. Following hydrolysis, the samples were cooled to room temperature, dried down in a speed vac and resuspended in 500 µl of methanol/water, 2:3 (v/v) containing 0.1% glacial acetic acid (solvent A).

Solid phase extraction on a Strata C18-E column.

The Strata C18-E solid phase extraction column (50 mg/ml) (Phenomenex, Torrance, CA) was initially wetted with 200 µl of methanol, followed by equilibration with 1 ml of solvent A. Fly extracts or LCB standards in solvent A were applied to the equilibrated Strata C18-E column, followed by a wash with 1 ml of solvent A. A second wash of the column was performed by the addition of 600 µl of methanol. LCBs were eluted from the column with 600 µl of methanol:10 mM ammonium acetate, 9:1 (v/v) and dried down in a speed vac.

HPLC Analysis

LCBs were derivatized with *ortho*-phthalaldehyde (OPA) (Sigma St. Louis, MO) as previously described (Caligan, T. B., K. Peters J. Ou, E. Wang, J. Saba, and A. H. Jr. Merrill. 2000. *Anal. Biochem.* 281: 36-44.). The OPA-derivatized LCBs were separated on a reverse-phase column (Luna RP-18, 3 μ, 4.6 x 75 mm) (Phenomenex, Torrance, CA) with the mobile phase methanol/10 mM ammonium acetate, pH 5.2, 82:18 (v/v). Flow rate was 1 ml/min. The HPLC system used was a Beckman System Gold with a 125 solvent module. The fluorescent LCBs were detected and quantified using a Spectra-Physics fluorescence detector (SP 8410).

Mass Spectrometry Analysis of Drosophila LCBs.

A Strata C18-E column-purified lipid extract from adult *Sphk2*^{KG05894} flies or a C_{14} So standard were analyzed on a Micromass Quattro LCZ instrument following direct injection of 10 μl of sample. Mobile phase was 80 percent methanol containing 0.1 percent formic acid. Flow rate was 0.2 ml/min. Structural confirmation of LCBs was obtained by positive electrospray ionization (ESI+) mass spectrometry. LCBs were detected by precursor ion scans of structurally distinct ion fragments as described (Sullards, M. C., and A. H. Jr. Merrill. 2001. *Sci. STKE.* **67:** 1-11.). Applying 3.5 kV to the capillary started the spray and the collision-induced decomposition spectra, at a cone voltage of 20 V, were recorded at a collision energy of 15 eV with argon as collision gas.

Abbreviations

So: sphingosine; Sa: didydrosphingosine, LCB: free long chain sphingoid bases; LCBP: phosphorylated free long chain sphingoid bases; SPT: serine palmitoyltransferase; OPA: ortho-phthalaldehyde.

Results:

HPLC Separation of Sphingoid Bases and Solid Phase Extraction of Sphingoid Bases

An HPLC method was developed for the separation of LCBs with a carbon number of 14 to 18. Initial HPLC separation of crude methanol/water lipid extracts from adult flies were complicated by high content of contaminating fluorescent material. Consequently, a solid phase extraction step using a Strata C18-E column prior to HPLC analysis was introduced. When methanol was employed as the eluting solvent, recovery of LCB standards was less than 2 percent. This inadequate recovery of the LCB standards from the Strata C18-E column was completely overcome by addition of 10 percent by volume of a 10 mM ammonium acetate solution to the methanol elution solvent. By employing this elution system, recovery in the range of 60 to 95 percent was obtained for the C_{14} and C_{16} sphingoid base standards (Table 3).

Table 3

Recovery of Sphingoid Base Standards Following Solid Phase Extraction on a STRATA C18-E column

Sphingoid base	C_{14} So	C_{16} So	C_{16} Sa	C_{18} So	C_{18} Sa
Recovery (%)	95.4 ± 3.3	77.9 ± 7.1	60.6 ± 4.2	39.3 ± 6.5	16.3 ± 4.0

Values are shown as mean ± standard deviation for at least three independent measurements.

HPLC Analysis of LCBs from *Drosophila*

Elution of adult fly lipids from the Strata C18-E column with methanol/10 mM ammonium acetate 9:1 (v/v) still resulted in an HPLC spectrum with significant unwanted background fluorescence. This background was minimized with the addition of a methanol wash prior to elution with methanol/10 mM ammonium acetate 9:1 (v/v) (see Materials and Methods for details). Adult flies of three different lines were analyzed. The lipid profile of wild type flies was compared to that of a sphingosine kinase (*Sphk2*) mutant and a serine palmitoyltransferase (SPT, *lace*) mutant (See Materials and Methods above). The *Sphk2* mutants would be predicted to manifest a reduced capacity to phosphorylate LCBs and as a consequence should demonstrate increased levels of LCBs. In contrast, the hypomorphic *lace* mutants are defective in the first step of sphingolipid *de novo* biosynthesis and would be predicted to exhibit diminished levels or complete absence of LCBs. Three peaks demonstrating the same retention times as the C_{14} So, C_{16} So and C_{16} Sa standards were identified in wild type fly extracts. In addition, a major peak that eluted with a retention time between that of C_{14} So and C_{16} So was identified. All four peaks mentioned above were increased in the *Sphk2* mutant and decreased in the *lace* mutant, consistent with the likelihood that these peaks represented LCBs. No peaks that eluted with retention times corresponding to the C_{18} LCB standards were observed.

Following isocratic elution from a C18 reverse phase HPLC column, a plot of the carbon length of a derivatized sphingoid base standard against the log of the retention time shows a linear correlation between sphingoid bases belonging to the same molecular class (Lester, R. L., and R. C. Dickson. 2001. *Anal. Biochem.* 298: 283-292.). This can be useful for the identification of an unknown sphingoid base. A linear correlation exists between the retention time of the unknown peak 2 and the two Sa standards in this plot. This finding strongly suggests that peak 2 is C_{14} Sa.

Mass Spectrometry Analysis of LCBs from *Drosophila*

LCBs can be identified through their patterns of collision-induced dissociation and precursor ion scans using positive ion electrospray mass spectrometry (ESI+). Based on their unique molecular structures, typical decomposition products arise from the loss of two water molecules. The precursor ion spectrum of m/z 208 (C_{14} So minus two water molecules) shows parents as m/z 244 (C_{14} So) and m/z 226 (C_{14} So minus one water molecule). In order to verify the existence of C_{14} Sa in *Drosophila*, we analyzed a Strata C18-E column purified lipid extract by ESI+. A lipid extract from the *Sphk2* mutant was chosen for the analysis since it demonstrated elevated levels of LCBs. Initially we sought the presence of endogenous C_{14} So. A precursor ion spectrum of m/z 208 identified C_{14} So (m/z 244) in the extract. Subsequently, we sought the presence of C_{14} Sa. A precursor ion spectrum of m/z 210 identified endogenous C_{14} Sa (m/z 246). In addition, precursor ion scans of m/z 236 and m/z 238 identified endogenous C_{16} So and C_{16} Sa in the fly extract. Precursor ion scans of m/z 264 and m/z 266 failed to identify C_{18} LCBs in the fly extract supporting the results obtained from the HPLC analysis.

C_{14} and C_{16} Sphingoid Bases in *Drosophila* Models of Sphingolipid Metabolism

Endogenous *Drosophila* LCBs were quantified by performing HPLC separation of Strata C18-E column purified extracts either with or without the addition of a defined amount of C_{14} So, C_{16} So and C_{16} Sa standard. Separation was followed by comparison of the integrated area obtained for each fluorescent LCB peak (Table 4). Interestingly, *lace* and *Sphk2* mutant flies differed appreciably from wild type flies in both the total amount and composition of LCBs, as determined by analysis of lipid extracts from each line. The total amount of LCBs in the wild type was approximately 1.5 nmol/100 mg of whole flies. The *Sphk2* mutants exhibited a 3.3 fold increase and the *lace* mutants, a 2.5 fold decrease in

the total amount of LCBs in comparison to wild type flies. C_{14} So accounted for approximately 42 percent of the total amount of LCBs in the wild type flies, whereas C_{14} Sa accounted for approximately 47 percent. Therefore, the molar ratio of C_{14} So to C_{14} Sa was approximately 1:1. In the *Sphk2* mutant, the corresponding values were 26 percent C_{14} So and 67 percent C_{14} Sa resulting in a molar ratio of approximately 1:2.5, whereas in the *lace* mutant the corresponding values were 16 percent C_{14} So and 81 percent C_{14} Sa resulting in a molar ratio of approximately 1:5.

Table 4

HPLC Analysis of Endogenous LCBs in Various Adult *Drosophila* Lines

	Wild type	*Sphk2*	*lace*
C_{14} So (nmol/100 mg of flies)	0.637 ± 0.132	1.282 ± 0.144 (201.3)	0.100 ± 0.019 (15.7)
C_{14} Sa [(a)] (nmol/100 mg of flies)	0.718 ± 0.097	3.282 ± 0.361 (457.1)	0.496 ± 0.055 (69.1)
C_{16} So (nmol/100 mg of flies)	0.055 ± 0.007	0.160 ± 0.011 (290.9)	0.018 ± 0.002 (37.7)
C_{16} Sa (nmol/100 mg of flies)	0.051 ± 0.009	0.198 ± 0.026 (388.2)	n.d.
Total LCBs (nmol/100 mg of flies)	1.461 ± 0.245	4.922 ± 0.542 [b] (336.9)	0.614 ± 0.076 [c] (42.0)
C_{14} So/C_{14} Sa (mol: mol)	0.89	0.39	0.20

Values are shown as mean ± standard deviation for three independent measurements. Value n.d. means there was no detectable LCB at the amount of fly material analyzed. Numbers in parentheses represent percent of wild type.

[a] An estimated value for the recovery of C_{14} Sa from the Strata C18-E column was determined using the following formula; % recovery of C_{14} Sa = % recovery of C_{16} Sa x (% recovery of C_{14} So/% recovery of C_{16} So).

[b] Significantly different from wild type; $P < 0.001$.

[c] Significantly different from wild type; $P < 0.005$.

C_{14} Sphingoid Bases in *Drosophila* Development.

Genetic studies have implicated a role for sphingolipid intermediates in the process of development. However, quantification of these molecules throughout development has not been performed. To investigate whether a biochemical basis for the potential role of sphingolipid intermediates exists, we evaluated the endogenous C_{14} LCBs at different stages of *Drosophila* development (Table 5). The total amount of C_{14} LCBs remained fairly constant throughout the development of the wild type. However, developmental progress from early embryos to pupae was associated with a seven fold increase in the molar ratio of C_{14} So to C_{14} Sa.

Table 5

HPLC Analysis of Endogenous C_{14} LCBs in Different Stages of Wild Type *Drosophila* development

	Embryo (0-6 hr)	Embryo (6-12 hr)	Embryo (12-18 hr)	Embryo (18-24 hr)	Larvae	Pupae
C_{14} So (nmol/100 mg of material)	1.210 ± 0.173	2.132 ± 0.359	1.616 ± 0.261	1.713 ± 0.072	3.328 ± 0.318	2.094 ± 0.126
C_{14} Sa (nmol/100 mg of material	1.156 ± 0.122	1.010 ± 0.098	0.461 ± 0.051	0.387 ± 0.012	0.722 ± 0.033	0.309 ± 0.047
Total C_{14} LCBs (nmol/100 mg of material)	2.366± 0.295	3.142± 0.457	2.077± 0.312	2.100 ± 0.084	4.050± 0.351	2.403 ± 0.173
C_{14} So/C_{14} Sa (mol: mol)	0.97	2.11	3.51	4.43	4.61	6.78

Values are shown as mean ± standard deviation for three independent measurements.

EXAMPLE 12

ANALYSIS OF GROSS AND MICROSCOPIC TUMOR DEVELOPMENT IN *DROSOPHILA MELANOGASTER* STRAINS WITH ALTERED SPHINGOLIPID METABOLISM

Some *Drosophila melanogaster* sphingolipid metabolic mutants may develop tumors, especially those which demonstrate significant accumulation of S-1-P. Previously characterized *Drosophila melanogaster* tumors associated with *lgl* and *dlg* mutations possess characteristics associated with neoplastic growth in vertebrates, including lethality to the host, repeated transplantability, invasiveness, absence of terminal differentiation, rapid growth *in vivo* and in tissue culture, and defective cell-cell interactions and communication. Evaluation of each of these characteristics in grossly or microscopically visible tumors arising in mutants is performed. Overgrowth of imaginal discs is sought in all mutants even in the absence of gross tumors. Lethal mutations may suggest the presence of tumor formation during early developmental stages. The ability of cells of imaginal disc tumors or imaginal disc overgrowth to respond to normal differentiation signals during metamorphosis is evaluated by transplanting mutant imaginal discs into wild type larvae and following their fate. The ability of tumors or hyperproliferative imaginal discs to be serially cultured *in vitro* and in the abdomens of adult females for numerous transfer generations is assessed. Evidence of tumor invasiveness and metastatic capacity will be determined by determining the presence or absence of invasion into tissues surrounded by an epithelial sheath using histological analysis.

EXAMPLE 13

ASSESSMENT OF GROSS AND MICROSCOPIC ANATOMIC DEFECTS IN *DROSOPHILA MELANOGASTER* STRAINS WITH ALTERED SPHINGOLIPID METABOLISM

Certain illustrative experimental methods are described herein, for example the above section before Example 1. Further illustrative techniques that can be used to further define the present invention, for example general

techniques for assessment of gross and microscopic anatomical defects of *Drosophila melanogaster*, are known in the art and are further described herein. Lifespan of each line is determined and compared to wild type flies to assess effects on viability. Gross anatomy of tracheal and muscular systems is viewed in larvae with polarized light and in adults by viewing standard thick sections under light microscopy, in order to identify gross defects affecting trachea or muscle number, size, location or proper attachment. Preparation for light microscopy involves storing flies in a glycerol/ethanol solution, followed by 70% ethanol, dissecting away unnecessary structures, rehydrating and mounting or embedding the specimen for sectioning. Visualization is be performed using bright-field, DIC illumination, phase contrast or dark-field illumination. Electron microscopic analysis of the IFMs is performed on adults, larvae and pupae. The early *Drosophila melanogaster* embryo is amenable to structural analysis using any of a large number of highly specific antibodies which is detected using fluorescent secondary or, in some cases, primary antibodies. Large numbers of staged embryos can be collected from normal and mutant stocks and prepared for fluorescent analysis. This process involves dechorionation using a bleach solution, permeabilizing the vitelline membrane, fixation (without methanol) and vitelline membrane removal, staining, washing and mounting. Since *lace* mutants demonstrate abnormal apoptosis of imaginal wing discs, we plan to investigate any changes in imaginal disc structure and eversion in all mutants. Dissection of imaginal discs is performed in a saline solution and involves tearing the third instar larva in half, inverting the body wall and pinching clusters of dorsal or ventral discs away from the body. Discs may be left attached to the body wall for *in situ* hybridization studies, or they may be removed and fixed for other studies. Pupal imaginal discs can also be isolated by removing the cuticle after fixation overnight.

EXAMPLE 14

IDENTIFICATION OF PHARMACOLOGIC SUPPRESSORS OF SPL MUTANT'S INABILITY TO FLY BY SCREENING AN ARRAY OF RATIONALLY DESIGNED CHEMICALS WITH HOMOLOGY TO SPHINGOLIPIDS FOR THEIR ABILITY TO RESTORE FLIGHT TO SPL MUTANT PROGENY

Pharmacologic suppressors of the *Sply* mutant *Drosophila melanogaster*'s inability to fly are identified by screening an array of rationally designed chemicals with homology to sphingolipids for their ability to restore flight to the *Sply* mutant *Drosophila melanogaster*. Mutant SPL flies are grown at 18^0 C in media supplemented with either vehicle control or micromolar concentrations of inhibitor. The ability of various inhibitors to restore flight will be measured using a standard scoring method, also as described elsewhere herein (see also Vigoreaux, et al., 1993, J Cell Biol 121:587-598). The efficacy and biochemical characteristics of interesting compounds will then be quantified by 1) determining the IC_{50} of the inhibitor on purified SK, SPL and other enzymes involved in sphingolipid metabolism, such as serine palmitoyltransferase, ceramide synthase, sphingosine desaturase, ceramidase, ceramide kinase, phosphoethanolamine cytidylyltransferase, CDP-ethanolamine phosphotransferas, acid sphingomylelinase and neutral sphingomyelinase. The IC50 of the inhibitor is also determined on recombinant human SK, SPL and other enzymes involved in sphingolipid metabolism as listed above; 2) analyzing the kinetics of inhibition using classical Michaelis-Menten methods, and 3) determining the reversibility of the inhibition.

Synthetic analogs are created for the screen. A library of 1-aryl-2-dimethylaminopropane-1,3-diol derivatives for screening as potential SK inhibitors are synthesized. Four diastereomers (D or L, *erythro* or *threo*) are synthesized for each member of the library. In the library the fatty acid amide group is replaced with two N-methyl groups and make similar variations in the polar and aromatic substituents. The synthetic plan makes use of the well-known Garner aldehyde (See **1** in Figure 2) as starting material, since **1** is readily available in either

enantiomeric form. A recent and exhaustive review of organometallic additions to **1** summarizing the effects of metal, solvent, and added Lewis acid catalyst has been published, and indicates that the *erythro*-product is usually favored in most reactions. Thus, by choosing the D- or L-enantiomer of **1** as starting material, pure *erythro* stereoisomers of each library member are prepared. A novel and flexible route for assembling the corresponding *threo* analogues (**4a-c**, Figure 2) is carried out using a straightforward extension of methodology for making PDMP analogues. The parent compound, **4a**, is already known and readily available. The strategy relies on the *syn*-selective addition to **1** of arylmetal compounds (Aryl-Met) in the presence of certain sulfide and phosphine additives. Both the *erythro* and *threo* synthetic routes are modified to prepare substituted variations at the primary carbon atom. A representative synthetic procedure is shown in Figure 3 for the preparation of **7a-c**. A wide range of nitrogen, oxygen, and carbon nucleophiles could react with mesylates like **5a-c** to furnish new libraries of dimethylated PDMP analogues and homologues.

EXAMPLE 15

FURTHER EVALUATION OF CANDIDATE DRUGS BY TESTING THEIR ABILITY TO INHIBIT HUMAN SK IN A YEAST SCREEN DEVISED SUCH THAT INHIBITION OF SK CONFERS CELL SURVIVAL

Compounds identified in the fly screen as described in Example 14 are further evaluated for their ability to inhibit human SK in a yeast model. Compounds which block the activity of human SK should restore growth on galactose to yeast strain *dpl1ysr2lcb4* (Gal1,10p:human SPHK1). This strain cannot catabolize S-1-P or endogenous yeast S-1-P analogs due to the deletion of genes encoding SPL and S-1-P phosphatases. The endogenous yeast SK gene, *LCB4* has also been deleted, so that no endogenous S-1-P analogs are made under baseline conditions. This strain has been transformed with a plasmid containing the human SPHK1 gene under regulation of a galactose inducible

promoter, such that expression of an active SK in the presence of galactose is lethal to this strain. Inhibition of human SK protects cells from galactose-induced lethality and confirms the efficacy of the compound in question. Activity of the human SPHK1 gene in this strain has been verified by two methods, first HPLC analysis of SK activity in whole extracts of cells grown (for a limited time) in the presence of galactose, and second, the inability of this strain to form colonies on galactose-containing plates.

D-*erythro*-sphingosine, N,N-dimethylsphingosine, and D,L-*threo*-dihydrosphingosine are obtained from Biomol Research Inc. (Plymouth Meeting, PA). The morpholine, piperadine and *erythro* series of PDMP analogues is obtained. Other analogues are prepared as described above and according to previously described methods (Srivastava, M., L. Bubendorf, V. Srikantan, L. Fossom, L. Nolan, M. Glasman, X. Leighton, W. Fehrle, S. Pittaluga, M. Raffeld, P. Koivisto, N. Willi, T.C. Gasser, J. Kononen, G. Sauter, O.P. Kallioniemi, S. Srivastava, and H.B. Pollard. 2001. ANX7, a candidate tumor suppressor gene for prostate cancer. *Proc Natl Acad Sci U S A*. 98:4575-4580.; Bockmuhl, U., S. Schmidt, S. Petersen, and I. Petersen. 2000. [Deletion of chromosome 10q--a marker for metastasis of head-neck carcinomas?]. *Laryngorhinootologie*. 79:81-85.; Morita, R., S. Saito, J. Ishikawa, O. Ogawa, O. Yoshida, K. Yamakawa, and Y. Nakamura. 1991. Common regions of deletion on chromosomes 5q, 6q, and 10q in renal cell carcinoma. *Cancer Res*. 51:5817-5820.; Jenkins, R.B., I.D. Hay, J.F. Herath, C.G. Schultz, J.L. Spurbeck, C.S. Grant, J.R. Goellner, and G.W. Dewald. 1990. Frequent occurrence of cytogenetic abnormalities in sporadic nonmedullary thyroid carcinoma. *Cancer*. 66:1213-1220.; Shen, W.P., R.F. Young, B.N. Walter, B.H. Choi, M. Smith, and J. Katz. 1990. Molecular analysis of a myxoid chondrosarcoma with rearrangements of chromosomes 10 and 22. *Cancer Genet Cytogenet*. 45:207-215.; Simpson, N.E., K.K. Kidd, P.J. Goodfellow, H. McDermid, S. Myers, J.R. Kidd, C.E. Jackson, A.M. Duncan, L.A. Farrer, K. Brasch, and et al. 1987. Assignment of multiple endocrine neoplasia type 2A to chromosome 10 by

linkage. *Nature*. 328:528-530.; Ichimura, K., E. Schmidt, A. Miyakawa, H. Goike, and V. Collins. 1998. Distinct patterns of deletion on 10p and 10q suggest involvement of multiple tumor suppressor genes in the development of astrocytic gliomas of different malignancy grades. *Genes Chromosomes Cancer*. 22:9-15.; Kim, S., H. Fyrst, and J. Saba. 2000. Accumulation of phosphorylated sphingoid long chain bases results in cell growth inhibition in *Saccharomyces cerevisiae*. Genetics. 156:1519-1529.).

Lipid extraction is carried out by Ion-exchange chromatography and HPLC analysis. SK assays are performed essentially as described (Taylor, M.V. 2000. Muscle development: molecules of myoblast fusion. *Curr Biol*. 10:R646-648.). Purification of native and recombinant SK is performed essentially as described Mao, C., M. Wadleigh, G. Jenkins, Y. Hannun, and L. Obeid. 1997. Identification and characterization of Saccharomyces cerevisiae dihydrosphingosine-1-phosphate phosphatase. *J Biol Chem*. 272:28690-28694).

EXAMPLE 16

GENERATION OF A TRANSGENIC *DROSOPHILA MELANOGASTER* EXPRESSION HUMAN SPL AND HUMAN SPL-GFP FUSIONS

Transgenic *Drosophila melanogaster* were generated that overexpress human SPL (cDNA set forth in SEQ ID NO:23; amino acid sequence set forth in SEQ ID NO:18) and human SPL-GFP fusion proteins using standard techniques as described herein. The transgenes were introduced into wild type Canton-S (BL-1), and *Sply*^{05091} (BL-11393), mutant fly backgrounds.

EXAMPLE 17

DEVELOPMENT OF A YEAST MODEL SYSTEM FOR SCREENING SK INHIBITORS

A yeast model system was developed that can be used as a screen to identify inhibitors of SK. A collection of yeast mutants demonstrating defects of long chain phosphorylated sphingoid bases (LCBPs) synthesis and metabolism

was created. These mutants provide a novel schema by which to elucidate LCBP metabolism and identify genetic suppressors. These same mutant yeast strains can be used to screen chemicals which influence LCBP metabolism through their effect on key enzymes in the LCBP metabolic pathway.

Yeast strains which contain a null allele of DPL1, the yeast sphingosine phosphate lyase (SPL) gene, are unable to grow in the presence of even very low concentrations of D-*erythro*-sphingosine added to growth media. Not to be bound by theory, this is presumed to be caused by the fact that sphingosine is rapidly phosphorylated to S-1-P, which subsequently accumulates due to the failure of *dpl1* mutant strain to catabolize the phosphorylated sphingoid base. This phenotype can be utilized to isolate mutants which cannot accumulate S-1-P and, therefore, are resistant to D-*erythro*-sphingosine. Mutations in the SK gene leading to diminished SK activity would reduce or eliminate production of S-1-P. Therefore, sphingosine resistant suppressors of *dpl1*Δ were selected in order to isolate SK-deficient mutants.

To ensure that deletion of *DPL1* has no effect on SK activity, the SK activity present in wild type and *dpl1*Δ strains was evaluated. No significant differences in the SK activity of these two strains were observed, indicating that *S. cerevisiae* SK was not subject to end product inhibition *in vivo*.

A population of *dpl1Δ* cells was then subjected to a selection on D-*erythro*-sphingosine-enriched plates in order to isolate spontaneous suppressors of sphingosine sensitivity. Utilizing this approach, a number of suppressor mutants were isolated that exhibited significantly greater resistance to the growth-inhibitory effects of sphingosine than the original *dpl1Δ* cells. To determine whether these putative SK mutants were capable of phosphorylating a sphingoid base substrate, several clones were incubated with 100 μM D-*erythro*-sphingosine and extracts from these clones were subjected to S-1-P measurements using an HPLC-based assay essentially as described in Caligan, T.B., *et al.*, 2000, *Analytical Biochemistry* 281:36-44. The strain in which the selection was performed (*dpl1Δ*)

is unable to catabolize S-1-P and, therefore, accumulated S-1-P when exposed to exogenous sphingosine. Sphingosine resistant mutants of *dpl1Δ* synthesized no detectable S-1-P, indicating that SK activity was absent. Subsequent to the genetic screen described above, transposon mutagenesis was employed in a new screen in which *dpl1* cells were transformed with a plasmid containing a transposable element, and the genomic location of the suppressor gene into which the transposon had inserted was determined. This approach led to the isolation of *LCB4* as the major yeast sphingosine kinase gene (*Saccharomyces cerevisiae* gene and protein sequences are available at www.yeastgenome.org). In further experiments, *LCB5*, a homologue of *LCB4* was identified as a minor yeast sphingosine kinase gene.

Subsequent to the isolation of *DPL1* as the yeast SPL gene and *LCB4* and its homologue *LCB5* as the yeast sphingosine kinase genes (Nagiec, M., *et al.*, *J Biol Chem* 1998, 273(31), 19437-19442; Lanterman, M. & Saba, J. *Biochemical J.* 1998, 332(2), 525-531.) two additional genes of sphingolipid metabolism were identified and characterized in yeast (Mao, C., *et al.*, *J Biol Chem* 1997, 272(45), 28690-28694; Mao, C., *et al.*, 1999, **342,** 667-675; Mandala, S.M., *et al.*, *Proc Natl Acad Sci U S A.* 2000 Jul 5;97(14):7859-64). These genes, *YSR2* and *YSR3*, encode the major and minor sphingosine phosphate phosphatases, which catalyze the dephosphorylation of LCBPs to LCBs. These genes were identified through their ability, when overexpressed, to allow the *DPL1* strain to survive in the presence of sphingosine. *SUR2* catalyzes conversion of dihydrosphingosine to phytosphingosine and was also recently cloned using yeast genetic approaches.

To further explore the biological roles of LCBPs, disruption mutants for *LCB4, LCB5, DPL1, YSR2, YSR3,* and *SUR2* were created, essentially as described in Kim, S., *et al.*, 2000 *Genetics.* 156:1519-1529. An HPLC method was adapted to measure intracellular concentrations of the phosphorylated long chain bases in a variety of yeast mutants carrying single or multiple null alleles in

the genes described above (Caligan, T.B., *et al.*, 2000, *supra*). Mutants were grouped according to those which either accumulated or lacked LCBPs. Double mutants of *dpl1* and *ysr2* were inviable, while triple mutants of *dpl1, ysr2*, and *lcb4* were viable. Further, growth inhibition associated with accumulated phosphorylated long chain bases was observed in the triple mutant *dpl1 ysr2 lcb4* overexpressing *LCB4*, utilizing the pYES2 plasmid, in which gene expression was activated in the presence of galactose but inhibited in the presence of glucose. These results indicated that phosphorylated long chain bases inhibited cell growth. Mutants defective in both *YSR2* and *SUR2*, which accumulated dihydrosphingosine 1-phosphate only, grew poorly. The phenotypes of the *ysr2 sur2* mutants were suppressed by overexpression of *DPL1*.

These results suggested according to non-limiting theory that elevated levels of phosphorylated long chain bases had an antiproliferative effect in yeast and that this phenomenon could be regulated by the presence or absence of SK activity within the yeast cell.

To help elucidate the mechanism of growth inhibition induced by LCBP accumulation, growth in the presence of galactose was then utilized as a method for selecting suppressor strains in order. This screen was successful in identifying several interesting genetic suppressors of LCBP accumulation. To discern such interesting suppressors and avoid repeatedly identifying SK mutants as suppressors of LCBP degradation mutants, a *LCB4-LacZ* fusion allele was used, which allowed the determination of which suppressors maintained SK expression as shown by blue colonies in the presence of IPTG and X-gal in the media. Colonies which gave a blue color in the presence of IPTG and X-gal, which grew on galactose-containing plates (which induced *LCB4* expression) and which were prototrophic for leucine (the marker present in the transposon used in the screen) were considered interesting isolates which had not lost the SK gene.

Yeast SK activity demonstrated biochemical characteristics quite distinct from those of human SPHK1. Although yeast SK was able to

phosphorylate both yeast and mammalian sphingoid bases, yeast SK was not inhibited by the mammalian SK inhibitor D,L-*threo*-dihydrosphingosine. Therefore, in order to validate two yeast genetic screens designed for the identification of inhibitors of human SK, it was necessary to create yeast strains which expressed human SPHK1 and which lacked yeast SK activity. Human SK cDNA (the human SK cDNA is set forth in SEQ ID NO:22, encoding the amino acid sequence set forth in SEQ ID NO:21) was synthesized by reverse transcription from total RNA obtained from human umbilical vein endothelial cells (HUVECs), and this fragment was cloned into the yeast expression vector pYES2 (Invitrogen, Carlsbad, CA), in which genes were expressed in a regulated fashion under control of a galactose inducible promoter as follows: Total RNA was extracted from HUVECs using the RNeasy Kit (Qiagen, Inc., Santa Clarita, CA), according to the manufacturer's instructions. Total RNA was utilized to create cDNA using reverse transcriptase and an oligo dT primer at 42^0 C for 50 minutes. This cDNA was used as a template for amplification of the human SPHK1 cDNA sequence using primers 5'-ATATTAAGCTTATGGATCCAGCGGGCGGCCCC-3' (SEQ ID NO:40) and 5'-AGATCTAGATCATAAGGG-CTCTTCTGGCGG-3' (SEQ ID NO:41), corresponding to the first 21 nucleotides and the last 19 nucleotides of the SPHK1 cDNA. Taq polymerase and the following PCR cycling conditions were used for amplification: 40 cycles of 94^0 C for 30 seconds; 55^0 C for 1 minute; 68^0 C for 2 minutes; 68^0 C for 7 minutes. The resulting DNA fragment was linearized by digestion with *Eco* RI and *Xba* I and cloned into the pYES2 yeast expression vector (Invitrogen Inc., Carlsbad, CA), in which genes cloned into the multiple cloning site were expressed under the regulation of the *GAL4* glucose-repressible/galactose inducible promoter. This expression vector contained a *URA3* gene useful in the selection of transformants on the basis of uracil prototrophy.

This plasmid was used to transform two yeast strains, the first of which contained a null allele for *DPL1* and *LCB4* and was therefore SPL and SK

deficient, and a second strain which contained the aforementioned two null alleles and, in addition, a null allele for *YSR2*, therefore being additionally deficient in sphingosine phosphate phosphatase activity. The latter strain did not survive in the presence of SK activity, due to the massive accumulation of LCBPs. Transformants in each background were selected for uracil prototrophy.

These strains were analyzed and it was found that the SPHK1 gene was expressed and functional in yeast. First, whole cell extracts of the strains overexpressing mammalian SPHK1 genes demonstrated SK activity. Second, the triple knockout strain was streaked onto galactose plates and evaluated for its ability to survive. Lethality on galactose containing plates and normal growth on glucose plates were considered evidence for the expression of an active SK gene under galactose inducible regulation.

In summary, in this example, two important yeast mutant strains were created:

1. the first strain contained a null allele for *DPL1* and *LCB4* (and was therefore SPL and SK deficient) and was further transformed with either the mouse or human SPHK1 gene (see Figure 4). This strain, like the *dpl1* mutant, was highly sensitive to exogenous sphingosine and did not grow in culture medium containing 50μM sphingosine unless SK activity was blocked.

2. a second strain which contained the aforementioned two null alleles of strain 1 and, in addition, a null allele for *YSR2*, therefore being additionally deficient in sphingosine phosphate phosphatase activity (see Figure 5). This strain was further transformed to express human SPHK1 gene under the regulation of an inducible galactose promoter. Thus, this strain survived in glucose but did not survive in the presence of galactose (even in the absence of media containing sphingosine), unless SK activity was blocked.

The yeast strains identified herein provide a powerful tool for the isolation of genes involved in sphingolipid metabolism and signaling and a useful model with which to explore the role of phosphorylated sphingoid bases in

eukaryotic cells. Further, these strains afford a novel approach to the identification of mammalian SK inhibitors.

In summary, the experiments described herein show that significant accumulation of the S-1-P analogues (LCBPs) in *S. cerevisiae* caused cell death. This lethality in yeast was the *opposite* of the growth stimulatory effect of S-1-P in mammalian cells, permitting the creation of screens in which SK inhibition allows for the survival of mutants containing defects in LCBP catabolism.

Methods

For the experiments described herein, yeast media and genetic methods were standard, as described in Adams, A., *et al.*, 1998. Methods in Yeast Genetics. Cold Spring Harbor Laboratory Press, Plainview, NY. 177 pp. Yeast transformations were performed by the lithium acetate procedure (Ito, H., et al., 1983. *J. Bact.* 153:163-168). One step gene disruption or deletion procedures were employed to replace the endogenous genes with selectable PCR-amplified disruption constructs as described in Baudin, A., et al., 1993. *Nucleic Acids Res.* 21:3329-3330; Lorenz, M., et al., 1995. *Gene*. 158:113-117; Wach, A., et al., 1994. *Yeast.* 10:1793-1808. Yeast strains are isogenic derivatives of JK9-3d (*leu2-3, 112 ura3-52 rmel trp1 his4 HMLa*). Most of the strains are meiotic segregants of diploid JK9-3d made singly or multiply heterozygous for disruption constructs *dpl1Δ::KanMX*, *ysr2Δ::KanMX*, *ysr3Δ::KanMX*, *lcb4Δ::KanMX*, *lcb5Δ::KanMX*, and *sur2Δ::KanMX*.

For HPLC analysis of LCBPs, strains containing a *dpl1* allele can be grown for a short time periods in sphingosine before dying. To determine the S-1-P concentration of *dpl1, human SK* yeast in the presence of sphingosine with or without SK inhibitors, yeast cultures are incubated at a cell density of 5 x 10^7 cells/ml for 2 hours in the presence of sphingosine at 30°C. Cultures are washed twice in sterile water and once in YP prior to lipid extraction. Lipids are extracted essentially as described in Kim, S., et al., 2000. Genetics. 156:1519-1529. Briefly,

lipids are extracted by adding 5 ml of ice-cold MeOH followed by vortexing for 1 minute and tip sonication for 20 seconds. Extracts are centrifuged for 5 minutes in a tabletop centrifuge and the supernatant collected. A second extraction is performed on the pellet by adding an additional 5 ml ice-cold methanol followed by vortexing and sonication. The combined lipid extracts are then dried down in a speed vac, resuspended in 200 ml of 0.1M NH_4OH in MeOH, sonicated for 30 seconds in a bath sonicator and incubated for 1 hour at 37°C to allow for the hydrolysis of esterified acyl chains. Following hydrolysis, the samples are cooled to room temperature, dried down with a flow of N_2 and resuspended in 1 ml of EtOH:H2O:diethylether:pyridine(15:15:5:1).

EXAMPLE 18

DEVELOPMENT OF TWO SCREENS FOR SK INHIBITORS USING MUTANT YEAST STRAINS

As described above in Example 17, two yeast mutant strains were developed (see Figure 4 and Figure 5). In this Example, two screens using the above described mutant strains to identify inhibitors of SK are described.

Screen 1: (Figure 4)

Previous screens for suppressors of the *dpl1* strain's sensitivity have been performed on agar plates containing 50 µM D-*erythro*-sphingosine (Saba, J., et al., *J Biol Chem* 1997, 272(42), 26087). Since lipids disperse among cell membranes, the toxicity of sphingosine to this strain is dependent upon the number of cells plated, and therefore the concentration of sphingosine and cell concentration are both kept constant. A 96 well plate assay is used in which small, equal numbers of *dpl1* cells are placed into each well, and an array of candidate chemicals (as described herein, for example in the section entitled, AGENTS THAT MODULATE SPHINGOLIPID INTERMEDIATES AND/OR COMPONENTS OF SPHINGOLIPID METABOLISM AND/OR SIGNALING and essentially as described in Example 14) are diluted into the wells prior to incubation. Growth curves are determined by

inoculating synthetic complete media with logarithmically growing cells to an O.D.$_{600\ nm.}$=0.1, then following increase in optical density as a function of time. The lowest inhibitory concentration of sphingosine is determined. Controls for optimization include *dpl1* in sphingosine of various concentrations plus N,N-dimethylsphingosine or D,L-*threo*-dihydrosphingosine, and wild type cells in the presence and absence of these inhibitors.

This approach is then compared to the standard plate assay, utilizing two available SK inhibitors, N,N-dimethylsphingosine and D,L-*threo*-dihydrosphingosine (Yatomi, Y., et al., *Biochemistry* 1996, 35(2), 626-633; Stoffel, W. & Bister, K. *Hoppe-Seyler's Z Physiol Chem* 1973, 354, 169-181.) Concentrations of D-*erythro*-sphingosine that inhibit cell growth overnight (at 30^{0}C with shaking) are determined by measuring turbidity at OD_{600nm}. D-*erythro*-sphingosine concentrations that inhibit growth of a specific number of inoculated cells except in the presence of SK inhibitors are chosen as conditions for the screen. The assay is then validated in a *dpl1 lcb4 lcb5* strain containing mouse SphK1 cDNA (GenBank Accession No. AF068748) (Kim, S., Fyrst, H. & Saba, J. *Genetics* 2000, 156, 1519-1529). Candidate agents promoting growth of this strain in sphingosine are validated using survival assays on agar plates containing the agent. The efficacy and biochemical characteristics of interesting compounds are quantified by 1) determining the IC_{50} of the inhibitor on purified SK and recombinant human SK, 2) analyzing the kinetics of inhibition using classical Michaelis-Menten methods, 3) by determining the reversibility of the inhibition and 4) by comparing the LCBP accumulation of a *dpl1 human SK* strain treated with no inhibitor vs. treatment with a known SK inhibitors vs. treatment with the new compound. *In vitro* SK assays are performed using an HPLC based assay as described in Caligan, et al., (*supra*).

Screen 2: (Figure 5)

Screen 2 is carried out as described above for Screen 1 except for the use of media containing 2% galactose in place of 2% glucose as a carbon source during screening, and lacking sphingosine.

In order to validate the *dpl1Δ* screen on agar plates the strains created above are inoculated to a density of 1 x 10^4 cells per plate onto agar plates containing 100 μM D-*erythro*-sphingosine and 0.0015% NP40 (used as a dispersant). At these concentrations of sphingosine and this cell density, the *dpl1Δ* strains do not grow. Similarly, plates containing D-*erythro*-sphingosine *plus* known SK inhibitors are incubated for 3-5 days, and plates are inspected for sphingosine resistance. If it appears that the strain containing human SK can survive sphingosine in the presence of SK inhibitors, a dilutional assay provides semi-quantitative information on the degree of protection afforded by the known inhibitors. For the sphingosine dilutional assay, cells are grown to saturation for 2-3 days in liquid cultures and then resuspended in minimal medium, placed in the first row of a 96 well plate and diluted serially from 1:2 to 1:4000 across the plate. The cultures are then template-inoculated onto a control plate (rich medium) and a plate containing 50 μM sphingosine and 0.0015% NP40, plus or minus SK inhibitor (At this concentration of NP40, no effects on cell viability are observed.) Plates are then incubated at 30°C for 2 days and assessed visually for differences in growth.

Methods for yeast growth and genetics and measuring LCBPs are as described in the preceding examples.

EXAMPLE 19

BIOCHEMICAL ANALYSIS OF SK INHIBITORS

The biochemical characteristics of the SK inhibitors identified in the above described yeast screens are evaluated as follows.

IC_{50} on recombinant human SK and SK obtained from a variety of sources including human platelets, leukemia cell lines, breast cancer cell lines, normal human lymphocytes and crude yeast extracts expressing human, mouse, *Drosophila* and *C. elegans* SK cDNA is carried out using standard assays. Kinetics of inhibition using classical Michaelis-Menten methods are determined. The presence or absence of inhibitor phosphorylation is determined using standard assays. The effect on SK activity at baseline and in response to known SK inhibitors is determined using SK assays as described herein and in the art. The effect of inhibitor on intracellular levels of sphingosine, dihydrophingosine, S-1-P, DHS-1-P, ceramide and total phospholipids is determined using an HPLC-based assay (*In vitro* SK assays and all sphingolipid measurements are performed using an HPLC-based assay essentially as described in Caligan, *et al.*, 2000 *Analytical Biochemistry* 281:36-44). In addition to determining specificity for SK from the sources mentioned above, specificity for SK is determined by evaluating inhibitor effects on other lipid kinases (diacylglycerol kinase and PI3 kinase) and protein kinase C, which is inhibited by sphingosine. Mass measurements of sphingolipids are determined using a radioactive uptake thin-layer chromatography (TLC) assay. Activity against other enzymes in the sphingolipid metabolic pathway, including SPP, SPL, serine palmitoyl transferase (SPT) and ceramide synthase are evaluated using standard assays. Methods used for the above analyses are essentially as described in Caligan, *et al.*, 2000 *Supra*; Skrzypek, M, *et al.*, 1999 *J. Bacteriol.* 181:1134-1140; Kim S., *et al.*, 2000 *Genetics*, 156:1519-1529; Lanterman, M and Saba, J., 1998 *Biochem J*, 332:525-531.

EXAMPLE 20

BIOLOGICAL ANALYSIS OF SK INHIBITORS

The biological characteristics of the SK inhibitors identified in the above described yeast screens are evaluated as follows.

SK inhibitors identified using the screens as described herein are evaluated for dosage-dependent effects on the morphology, proliferation, apoptosis and stress response in cancer cell lines, including lines harboring dominant Ras mutations or SK overexpression (ovarian, colon, and breast cancer.) SK inhibitors are investigated for potential synergy with SPL overexpression in reducing S-1-P levels and signaling in a HEK293 cell line stably overexpressing a human SPL-GFP fusion protein. This cell line demonstrates very high SPL activity and increased apoptosis under stress conditions compared to a cell line stably expressing a catalytically inactive human SPL. Apoptosis in 0 - 10% serum is determined by caspase 3 activation. Information gained from these studies provides tools necessary to identify human SK inhibitors from any chemical array or library that might potentially contain them. In addition, compounds are tested for their ability to inhibit *Drosophila* SK function and to correct the physiological, anatomical, and reproductive defects of the *Drosophila* *Sply* mutant as described herein which lacks SPL expression.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purpose of illustration, various modifications may be made without deviating from the spirit and scope of the invention.